STIC-Biotech/ChemLib

Schnizer, Hol

From: Sent: To:

Subject:

Schnizer, Holly Tuesday, July 03, 2001 7:47 AM STIC-Biotech/ChemLib sequence search for appl. no. 09/490,291

Please search the commercial and interference databases for the following:

SEQ ID NO: 2, 4, 6, 8, 9 and 11

Themk you.

Holly Schnizer AU 1653 CM1-10B05 305-3722 RELATED 130086

45827

appl MB/MB/

Point of Contact:
Point of Contact:
Point of Contacts
Point of Sheckelist
Pool (No. Sheckelis

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GenCore version Copyright (c) 1993 - 2000

4.5 Compugen Ltd.

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein -
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                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB DB
                                                                                                                                                            279
243
                                                                                                                                                                                                                 Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein search, using sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length:
                                                                                                                                                                                                                 Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 July 3, 2001, 14:58:14; Search time 86.32 Seconds (without alignments) 51.971 Million cell updates/sec
74.
56.65
56.55
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                        SIDSB/gcgdata/geneseq/yeneseqp/AA1985.DAT:

SIDSB/gcgdata/geneseq/yeneseqp/AA1985.DAT:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412676 seqs, 60623988 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-490-291-11
377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRGSHHHHHHGSMASGDLKN.....AKIGDLNNTSGIRRPAAKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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                                AAB10562
AAB10561
AAW43025
AAW43026
AAW43027
AAB10558
AAW43028
AAW43024
AAB10557
                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               model
                                                                                                                                                                                                                 Description
                                                                                                                                                        Copolymer block pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
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	AAR39491	14	342	23.7	89.5	•
Human apoAIV mutei	AAR39489	14	342	23.7	•	.,
Human apoAIV mutei	AAR39487	14	342	23.7	•	_
His-tagged polylin	AAW61046	19	359	•	90	•••
Firbonectin-bindin	AAW31555	19	345	•	90	
OAIV mut	AAR39485	14	337	•	90	_
of nev	AAP90512	10	380	٠	•	_
of an	AAP90511	10	380		•	
of an	AAP90510	10	380	٠	90.5	-
of an	AAP90509	10	380	24.0	90.5	•
an	AAP90508	10	379	•	91	-
ř	AAB10560	21	18	•	91	_
e E	AAY44381	21	169	•	91:5	
P.aeruginosa E coi	AAY44385	21	168	24.3	۲.	•••
P. falciparum spor	AAR13992	12	493	•	92	
Collagen binding p	AAW31552	19	159	24.4	92	_
H6FXtripB-UB fusio	AAW94266	20	145	24.4	92	_
P. aeruginosa H co	AAY44382	21	175	•	94	-
Ξ	AAY44380	21	169	•	94	-
вно	AAY44384	21	168	•	94	
Human apoAIV mutei	AAR39486	14	373	25.2	95	-
	AAY44383	21	175	•	96	
Recombinant Sp 100	AAW13373	18	491	•	96.5	
Human caspase-8.	AAB59578	22	286	•	101.5	•
n procaspase	AAY56997	21	286	•	101.5	•
Zip5 polypeptide u	AAB08378	21	43	•	104	_
	AAB08386	21	43	•	111.5	_
Amino acid sequenc	AAB08366	21	43	•	113	_
Amino acid sequenc	AAB08362	21	43	30.0	113	-
D.	AAB08375	21	43	•	114.5	-
Amino acid sequenc	AAB08344	21	43	•		
HIV protease-assoc	AAB70796	22	93		118.5	
HIV protease-assoc	707	22	103	31.7	119.5	
Peptide used to as	AAB08383	21	43	32.1	121	

ALIGNMENTS

RESULT AAB10562

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AAB10562 standard;

protein;

76 Ą

15-DEC-2000

(first entry)

AAB10562;

integrin; fibroblast cell; matrix for antibiotic; dressing; abrasion; burn. Unidentified Coiled coil protein; copolymer blocker; vulnerary; wound treatment; integrin; fibroblast cell; matrix formation; skin regeneration; scaffold; Copolymer block protein insert L2-B Petka WA, 22-OCT-1997; 22-OCT-1997; 18-JUL-2000 US6090911-A (UYMA-) UNIV MASSACHUSETTS McGrath KP, 97US-0956307 97US-0956307 Tirrell DA;

221 213 205 205 199 197 181 181 124

AAW43029

Artificial recogni Coiled coil protei Artificial recogni Artificial recogni

WPI;

2000-542235/49.

Artificial recogni Artificial recogni

Coiled coil protei

Synthetic block copolymer with an antibiotic compound, useful for dressing abrasion, burn or non-puncture wound, comprises two alpha-helical protein blocks, random-coil protein block and linker proteins

Amino acid Amino acid

sequenc

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This invention describes a novel synthetic block copolymer XYZ comprising two alpha-helical protein blocks x and Z, a water soluble, random-coil converted by the converted block y which links x and Z, and linker proteins for linking the call protein block y which links x and Z, and linker proteins for linking the call protein block to the random-coil protein block. The copolymer helical protein blocks to the random-coil protein block. The copolymer produced in water to form a gel, which was then used to treat a wound. The cell coping to spria/IIIa proteins expressed on fibroblast cells necessary for matrix formation for the regeneration of skin. Fibroblasts become compared within the gel and thus remain at the site of the wound, copolymer so a scaffold for the regeneration of tissue surrounding the compound. A synthetic block copolymer together with an antiblotic compound is useful for wound dressing. The copolymer is useful for dressing the copolymers of equal size are produced biologically from a single template. The intermolecular binding of alpha-helical blocks are monodisperse which gives a uniform pore size depending on the length of random-coil block. The new copolymers have low molecular weight hence have decreased corposents a copolymer block protein L2-A which is used to illustrate the method of the invention.
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Best Local Similarity
Matches 57; Conser
                                                                                                                                                                                                                                                                                                               Coiled coil protein; copolymer blocker; vulnerary; wound treatment; integrin; fibroblast cell; matrix formation; skin regeneration; scaffold;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Synthetic block copolymer with an antibiotic compound, useful
                                WPI; 2000-542235/49
                                                                                                                                                                                                                                US6090911-A.
                                                                                                                                                                                                                                                                                                 antibiotic;
                                                                                                                                                                                                                                                                                                                                                                Copolymer block protein insert L2-A.
                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Column 33-36; 53pp; English.
                                                                Petka WA, McGrath KP,
                                                                                                 (UYMA-) UNIV MASSACHUSETTS
                                                                                                                                 22-OCT-1997;
                                                                                                                                                                22-OCT-1997;
                                                                                                                                                                                                18-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB10561 standard; protein; 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 kigd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 KIGD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRGSHHHHHHGS-----MASGDLKNKVAQLKRKVRSLKDKAAELKQEVSRLENEIEDLKA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76
                                                                                                                                                                                                                                                                                              dressing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽,
                                                                                                                                 97US-0956307
                                                                                                                                                                 97US-0956307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.18;
                                                                                                                                                                                                                                                                                                 abrasion; burn
                                                                  Tirrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 279.5; DB Pred. No. 1e-22; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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This invention describes a novel synthetic block copolymer XYZ comprising two alpha-helical protein blocks X and Z, a water soluble, random-coil coil protein block Y which links X and Z, and linker proteins for linking the CC alpha-helical protein blocks to the random-coil protein block. The CC products of the invention have vulnerary activity. A copolymer produced in water to form a gel, which was then used to treat a wound. The cell coinding domain was the integrin ArgGlyAspSer sequence which is known to bind to applia/IIIa proteins expressed on fibroblast cells necessary for commatrix formation for the regeneration of skin. Fibroblasts become company as a scaffold for the regeneration of skin. Fibroblasts become compound. A synthetic block copolymer together with an antibiotic compound is useful for wound dressing. The copolymer is useful for dressing companies and formation of non-puncture wound. Unlike conventional polymers, the polymers of equal size are produced biologically from a single template. The new copolymers have low molecular weight hence have decreased component or opplymers have low molecular weight hence have decreased component of the invention. This sequence method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dressing abrasion, burn or non-puncture wound, comprises two alpha-helical protein blocks, random-coil protein block and linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Column 33-34; 53pp; English
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₽ B δÃ Š Query Match Best Local Matches AAW43025 standard; Peptide; 84 :||| 61 eigd 64 56 KIGD 59 1 mrgshhhhhhgsddddkwasgdlenevaqlerevrsledeaaeleqkvsrlkneiedlka 60 1 MRGSHHHHHHGS-----MASGDLKNKVAQLKRKVRSLKDKAAELKQEVSRLENEIEDLKA 55 w 48; Similarity Conservative 64.6%; 75.0%; 10; Score 243.5; DB 21; Pred. No. 6.5e-19; Mismatches 1; Indels Length 5, Gaps ۲

Sequence

AAW43025 Artificial recognition sequence 08-MAY-1998 AAW43025; (first entry)

selectively Recognition spontaneous sequence; self-assembling; protein-based structural material; heterodimerisation; coiled-coil alpha helix; permeable membrane; coated fabric.

Kaplan DL, US5712366-A Synthetic (USSA) US SEC OF ARMY 25-MAY-1993; 25-MAY-1995; 27-JAN-1998 93US-0068948 95US-0452592

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RESULT
AAW43026
ID AAW4
XX AAW4
XX AAW4
XX O8-M
XX Reco
XW Reco
KW Spnt
XX Synt
XX Syn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subsequent genetic manipulations: The DNA sequence use a "mixed site" approach at the first base of the codons for amino acids positions 5 and 7 of the heptad (see below). The formation of a self-assembling structural material is mediated by the artificial recognition sequences (e.g. present sequence). A method of producing a self-assembling protein-based structural material comprises mixing a multiplicity of 2 different artificial peptide sequences, designed so as to spontaneously heterodimerise. Both artificial peptides have a coiled-coil spontaneously heterodimerise into a self-assembled call peptides spontaneously heterodimerise into a self-assembled protein-based structural materials. The method is used to produce nanoscale structural materials designed for specific functions e.g. membranes, fibres, absorbants, reactive materials, etc. A specific application is in the fabrication of selectively permeable membranes for hazardous materials. Materials for medical implants, wound healants and other medical treatments would also be feasible using this technology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 46
Production of peptide hetero:dimer(s) - in the fabrication self-assembling protein-based structural material(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    obtained by reverse translation. The codons were chosen to maximise expression in Escherichia coli, and to introduce useful restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5712366-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       selectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Production of peptide hetero:dimer(s) - in the fabrication of self-assembling protein-based structural material(s)
                                                                                                                                                                                                                                                                                                                                              25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW43026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-120029/11.
                                                                                                                                                                                                                      (USSA) US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW43026 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1998-120029/11
                                                                                                                                                       DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                      SEC OF ARMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                          McGrath KP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence; self-assembling; protein-based structural material;
heterodimerisation; coiled-coil alpha helix;
permeable membrane; coated fabric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent recognition sequences obtained from the library of sequence coded for by AAV04943. This DNA sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 1.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₿
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ARRESULT
ARAW4307
ID AAW
XX
AR AAW
XX
DT 08-h
DT 08-h
XX
Rec
KW Spot
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5712366-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           selectively
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Artificial recognition sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other medical treatments would also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                             self-assembling
                                                                                                                                                              Production of peptide hetero:dimer(s) - in the fabrication
                                                                                                                                                                                                                             WPI; 1998-120029/11.
                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recognition
                                                                                                                                                                                                                                                                                                                                                    (USSA ) US SEC OF ARMY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
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                                                                  Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence; self-assembling; protein-based structural material;
heterodimerisation; coiled-coil alpha helix;
permeable membrane; coated fabric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 4C; 17pp; English
                                                                                                                                                                                                                                                                                         McGrath KP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0452592
                                                                  4D;
                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0068948
                                                                                                                             protein-based structural material(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.5%;
93.6%;
                                                              17pp;
                                                                  English
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Pred. No. 1.2e-15;
2; Mismatches 1.
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AAW43024-28 represent recognition sequences obtained from the library of

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RESULT
AAB10558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Coiled coil protein; copolymer blocker; vulnerary; wound treatment; integrin; fibroblast cell; matrix formation; skin regeneration; sca antibiotic; dressing; abrasion; burn; Bl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recognition sequenes coded for by AAV04943. This DNA sequence is obtained by reverse translation. The codons were chosen to maximise expression in Escherichia coli, and to introduce useful restriction
                                                                                                                                              Synthetic block copolymer with an antibiotic compound, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coiled coil protein Bl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB10558 standard;
                                                                                                                                                                                                                                                                                    22-OCT-1997;
                                                                                                                                                                                                                                                                                                                   22-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                    18-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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                                                                                                                                                                                 2000-542235/49
                                                                                                                                                                                                                  WA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                             abrasion, bur
lical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                  97US-0956307
                                                                                                                                                                                                                                                                                                                   97US-0956307
                                                           25-26; 53pp; English
                                                                                                             burn or non-puncture wound, comprises ein blocks, random-coil protein block a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.48;
                                                                                                                                                                                                                  Tirrell DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 205; DB 19;
Pred. No. 8.6e-15;
4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scaffold;
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This invention describes a novel synthetic block copolymer XYZ comprising two alpha-helical protein blocks X and Z, a water soluble, random-coil protein block Y which links X and Z, and linker proteins for linking the

Example 1;

Column

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in water to form a gel, which was then used to treat a wound. The cell binding domain was the integrin ArgGlyAspSer sequence which is known to binding domain was the integrin ArgGlyAspSer sequence which is known to complete the proteins expressed on fibroblast cells necessary for matrix formation for the regeneration of skin. Fibroblasts become centrapped within the gel and thus remain at the site of the wound, serving as a scaffold for the regeneration of tissue surrounding the wound. A synthetic block copolymer together with an antibiotic compound is useful for wound dressing. The copolymer is useful for dressing cis useful for wound dressing. The copolymer is useful for dressing cis useful for wound dressing. The copolymer is useful for dressing cis useful for wound are produced biologically from a single template. The intermolecular binding of alpha-helical blocks are monodisperse which gives a uniform pore size depending on the length of random-coll block. The new copolymers have low molecular weight hence have decreased coviscosity solutions or gels under suitable conditions. This sequence represents the colled coil protein Bl which is used to illustrate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
AAW43024-28 represent recognition sequences obtained from the library recognition sequences coded for by AAV04943. This DNA sequence is obtained by reverse translation. The codons were chosen to maximise expression in Escherichia coli, and to introduce useful restriction for subsequent genetic manipulations. The DNA sequence use a "mixed site" approach at the first base of the codons for amino acids positions 5 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recognition sequence; self-assembling; protein-based structural material; spontaneous heterodimerisation; coiled-coil alpha helix; selectively permeable membrane; coated fabric.
                                                                                                                           Disclosure;
                                                                                                                                                                                Production
                                                                                                                                                                                                                                                                                                                           25-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                              25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                US5712366-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Artificial recognition sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW43028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW43028 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-helical protein blocks to the random-coil
                                                                                                                                                              self-assembling
                                                                                                                                                                                                                                                                                      (USSA ) US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 SGDLKNKVAQLKRKVRSLKDKAAELKQEVSRLENEIEDLKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ucts of the invention have vulnerary activity. A copolymer was a gene that encodes a derivative of AC_1_0A copolymer was
                                                                                                                                                                                                                   1998-120029/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L Similarity
42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention.
                                                                                                                                                                                                                                                                                        SEC
                                                                                                                                                                               of peptide hetero:dimer(s) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42
                                                                                                                         Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                        OF ARMY
                                                                                                                                                                                                                                                                                                                           9305-0068948
                                                                                                                                                                                                                                                                                                                                                              95US-0452592
                                                                                                                             4E;
                                                                                                                                                            eptide hetero:dimer(s) - in the fabrication
protein-based structural material(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide;
                                                                                                                                                                                                                                                      χ̈́P
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                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 199; DB 21; Pred. No. 1.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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ty. A copolymer produced
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                                      for
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RESULT
ANAMA3024
ID ANAMA
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XX Recc
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XX Syn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 40
AAW43024-28 represent recognition sequences obtained from the library of recognition sequence coded for by AAV04943. This DNA sequence is obtained by reverse translation. The codons were chosen to maximise expression in Escherichia coli, and to introduce useful restriction for subsequent genetic manipulations. The DNA sequence use a "mixed site" approach at the first base of the codons for amino acids positions 5 and 7 of the heptad (see below). The formation of a self-assembling structural material is mediated by the artificial recognition sequences (e.g. present sequence). A method of producing a self-assembling protein-based structural material comprises mixing a multiplicity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8661-AW-80
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                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4A; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            self-assembling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-120029/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaplan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Production
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Local Similarity 85.1%;
les 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DĽ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of peptide hetero:dimer(s) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McGrath KP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence; self-assembling; protein-based structural material;
heterodimerisation; coiled-coil alpha helix;
permeable membrane; coated fabric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-based structural material(s)
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6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
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Best Local S
Matches 36
products of the invention have vulnerary activity. A copolymer produced from a gene that encodes a derivative of AC_10A copolymer was suspended in water to form a gel, which was then used to treat a wound. The cell binding domain was the integrin ArgGlyAspSer sequence which is known to bind to gpITa/IIIa proteins expressed on fibroblast cells necessary for matrix formation for the regeneration of skin. Fibroblasts become entrapped within the gel and thus remain at the site of the wound, serving as a scaffold for the regeneration of tissue surrounding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spontaneously heterodimerise. Both artificial peptides have a coiled-coil alpha helical secondary structure having at least 2 heptad units. The artificial peptides spontaneously heterodimerise into a self-assembled protein-based structural material. The method is used to produce nanoscale structural materials designed for specific functions e.g. membranes, fibres, absorbants, reactive materials, etc. A specific application is in the fabrication of selectively permeable membranes for protective gloves and coated fabrics for fuel handlers and other hazardous materials. Materials for medical implants, wound healants and other medical treatments would also be feasible using this technology.
                                                                                                                                 This invention describes a novel synthetic block copolymer XYZ comprising two alpha-helical protein blocks X and Z, a water soluble, random-coil protein block Y which links X and Z, and linker proteins for linking the alpha-helical protein blocks to the random-coil protein block. The
                                                                                                                                                                                                                                                                   Synthetic block copolymer with an antibiotic compound, useful for dressing abrasion, burn or non-puncture wound, comprises two alpha-helical protein blocks, random-coil protein block and linke.
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                                                                                                                                                                                                                   Example 1; Column 25-26;
                                                                                                                                                                                                                                                    proteins
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                                                                                                                                                                                                                                                                                                                                                                                                   (UYMA-) UNIV MASSACHUSETTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     integrin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coil protein; copolymer blocker; vulnerary; wound treatment;
in; fibroblast cell; matrix formation; skin regeneration; sca
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Pred.
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Best Local :
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                                                                                                                                                                         Misc-difference
                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   method of
                                                      27-JAN-1998
             25-MAY-1993;
                                 25-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence giving a library of recognition sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   sequence; self-assembling; protein-based structural material;
heterodimerisation; coiled-coil alpha helix;
permeable membrane; coated fabric.
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             93US-0068948
                                 95US-0452592
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14
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                                                                                                                                                                                                                                                                                                                                     /note= "any chrged residue,
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                                                                                                                   note- "any chrged residue,
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76.2%;
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Pred. No. 2.
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self-assembling protein-based structural material(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Binding partner; protein modification; post-translational modification;
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                                                                                                                                                                                                                                                                                                                             Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modulator; coiled-coil structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a coiled-coil peptide.
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Pred. No. 1.4e-06;
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25-FEB-2000; 2000WO-GB00669

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RESULT 12
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                                                             High throughput assay for monitoring modification of polypeptides and modulation of the modifications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding partner; protein modification; modulator; coiled-coil structure.
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Example 9; Page 80; 128pp; English.
                                                                                                                                                       WPI; 2000-572119/53
                                                                                                                                                                                                              Colyer J,
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                                                                                                                                                                                                                                                                         (FLUO-) FLUORESCIENCE LTD.
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                                                                                                                                                                                                              Craig RK,
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                                                                                                                                                                                                              Maschio A,
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Pred. No. 3.1e-06;
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                                                                                                                                         Disclosure;
                                                                                                                                                                                             protease substrate useful for measuring protease activities and in online screening assays for proteases or protease inhibitors, comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV protease-associated protein #2.
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                                                                                                                                        Fig 2; 14pp;
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                                                                                                                                                                                   cleavage site and
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This invention describes a novel protease substrate for detecting a target protease which comprises a polypeptide containing a high-affinity binding site (1) for binding to a support, a cleavage site (2) specific for the target protease, and a sequence of amino acids forming a stretched helix (3). The substrate is useful for measuring protease activities and in online screening assays for proteases or protease inhibitors, especially based on surface plasmon resonance.

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease substrate useful for measuring protease activities and in online screening assays for proteases or protease inhibitors, comprises a polypeptide with a binding site, a cleavage site and a stretched helix -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 14pp; German
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                                                                               HHHHHHGSMAS----GDLKNKVAQLKRKVRSLKDKAAELKQEVSRLEN-----EIEDLK 54
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                      AKIGDL-NNTSGIRRPAAKL 73
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                                                                                                                                                  31.4%; Score 118.5; DB 22. 32.5%; Pred. No. 1.4e-05; Live 20; Mismatches 23;
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Pred. No. 1.2e-05;
Pred. No. 1.2e-05;
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                                                                                                                                                                                          DB 22;
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                                                                                                                                                                                            Length 93;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 21;
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                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                     the method of the invention.
                                                                  5 HHHHHHGSMASGDLKNKVAQLKRKVRSLKDKAAELKQEVSRLENE 49
Similarity
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                                                                                                                              30.5%; Score 115; DB 21;
44.4%; Pred. No. 1.3e-05;
tive 14; Mismatches 9;
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Maximum DB
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1: /cgn2_6/ptodata/2,
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Match
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Gapop 10.0 ,
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     US-08-956-307B-18
US-08-956-307B-17
US-08-452-592B-8
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US-08-452-592B-10
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US-08-452-592B-11
US-08-456-307B-1
US-08-956-307B-1
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US-08-956-307B-4
US-08-956-307B-3
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US-08-68-34BA-12
US-08-68-34BA-12
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US-08-680-87-33-33-13
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Query Match
Best Local Similarity 89...
Matches 57; Conservative

74.18; 89.18;

Score 279.5; DB 3; Pred. No. 1.7e-23; 1; Mismatches 1;

Indels Length

Gaps

76; 5;

APPLICATION NUMBER OF THE APPLICATION NUMBER OF TONNEY AGENT IN NAME: Fasse, J REGISTRATION NUMBER OF TRAINING AND ARBERT OF TRAINING ARBERT OF TRAINING AND ARB	GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Petka, Wendy A. APPLICANT: Tirrell, David A. APPLICANT: Kevin P. McGrath TITLE OF INVENTION: REVERSIBLE HYDROGELS NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston CITY: Boston STATE: MA COUNTRY: USA COUNTRY: USA ZIP: 02110-2804 COMPUTER READABLE FORM: COMPUTER: HAM Compatible OPERATING SYSTEM: Windows 95 SOFTWARE: FastSEO for Windows Version 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/956,307B FILING DATE: 22-OCT-1997 DEFOR ADDITORNION DATA:	ALIGNMENTS RESULT 1 US-08-956-307B-18 Sequence 18, Application US/08956307B	28 79 21.0 254 4 US-09-004-731-89 29 79 21.0 254 4 US-09-004-731-92 30 79 21.0 254 4 US-08-749-659-89 31 79 21.0 254 4 US-08-749-659-89 32 79 21.0 351 2 US-08-701-91A-3 33 79 21.0 532 3 US-08-737-336-6 34 79 21.0 631 1 US-08-659-541B-12 35 78.5 20.8 98 2 US-08-690-011A-19 36 78 20.7 16 1 US-08-690-011A-19 37 78 20.7 20 4 US-08-690-011A-19 38 78 20.7 20 4 US-08-640-737-32 39 78 20.7 35 2 US-08-491-527A-2 40 78 20.7 35 2 US-08-845-659-2 41 78 20.7 184 3 US-08-65-307B-19 42 78 20.7 184 3 US-08-676-318A-34 44 75 19.9 12 5 PCT-US94-09700-4 45 75 19.9 20 2 US-08-543-020-12
			Sequence 89, Appl Sequence 92, Appl Sequence 92, Appl Sequence 92, Appli Sequence 3, Appli Sequence 12, Appli Sequence 13, Appli Sequence 13, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 30, Appli Sequence 31, Appli Sequence 31, Appli Sequence 32, Appli Sequence 33, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 44, Appli

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; LENGTH: 76 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-956-307B-17
                                                                                   US-08-452-592B-7
                                                                                                     RESULT
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US-08-956-307B-17
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                               Sequence 7, Application US/08452592B Patent No. 5712366 GENERAL INFORMATION:
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Best Local Similarity
Matches 48; Conserv
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Patent No. 60909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0788
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 76 amino acids
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OPERATING SYSTEM: Windows 95
OPERATE FAST-SEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,307B
FILING DATE: 22-OCT-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Petka, Wendy A.
APPLICANT: Tirrell, David A.
APPLICANT: Kevin P. McGrath
TITLE OF INVENTION: REVERSIBLE HYDROGELS
NUMBER OF SEQUENCES: 24
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
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TELEFAX: 200154
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                                                                                                                                                      61 EIGD 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                          1 MRGSHHHHHHGS-----MASGDLKNKVAQLKRKVRSLKDKAAELKQEVSRLENEIEDLKA 55
                                                                                                                                                                                                                        MRGSHHHHHHGSDDDDKWASGDLENEVAQLEREVRSLEDEAAELEQKVSRLKNEIEDLKA 60
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McGrath, Kevin P.
Kaplan, David L.
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                          64.68;
75.08;
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                                                                                                                                                                                                                                                                                                          Score 243.5; DB 3
Pred. No. 1.3e-19;
                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                          DB 3;
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Patent No. 5712366
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 34,857 (I
REGISTRATION NUMBER: 29,579 (I
REFERENCE/DOCKET NUMBER: NA-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-233-4510
TELEPHONE: 508-233-5167
                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. Army Soldier Systems
                                                                                                                                                                                                                                                                APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using
TITLE OF INVENTION: Self-Assembling Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/06
FILING DATE: 25 May 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WordPerfect Version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,592B
FILING DATE: 25 May 1995
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MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: IBM PC Compatable
OPERATING SYSTEM: DOS 6.22
SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          APPLICANT: McGrath, Kevin P. APPLICANT: Kaplan, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE
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                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                  MEDIUM TYPE: Diskette, 3.50
COMPUTER: IBM PC Compatable
OPERATING SYSTEM: DOS 6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 GDLKNKVAQLKRKVRSLKDKAAELKQEVSRLENEIEDLKAKIGDLNN 62
                                                                                                                                                                    CITY: Natick
                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America ZIP: 01760-5035
                                                                                                                              COUNTRY:
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                                                                                                                : Massachsuetts
RY: United States of America
01760-5035
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Lamming, John H.
Ranucci, Vincent J.
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DE ADDRESS:
OU.S. Army Soldier Systems Command
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.6%;
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                    Version 6.1
                                                                        3.50 inch,
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Pred. No. 3.7e-17;
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                                                                            2.0 MB storage
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

08/068,948

APPLICATION NUMBER: FILING DATE: 25 Ma CLASSIFICATION: 53

US/08/452,592B 1995

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COUNTRY: United COUNTRY: COUNTRY: United COUNTRY: COUNTRY: United COUNTRY: 01760-5035

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
COMPUTER: IBM PC Compatable
COMPUTER: IBM PC Compatable
OPERATING SYSTEM: DOS 6.22
SOFTWARE: WOTGOPERATE Version 6.1
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/08/452,592B
TILING DATE: 25 May 1995
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Best Local Similarity
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                                                                                                                                                             FILING DATE: 25 May 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/068,948
FILING DATE: 25 May 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
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TELEPHONE: 508-233-4510
TELEFAX: 508-233-5167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using
TITLE OF INVENTION: Self-Assembling Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 25 May 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
                   NAME: Donahue, Richard J.

NAME: Lamming, John H.

NAME: Ranucci, Vincent J.

REGISTRATION NUMBER: 22,062 (Donahue)

REGISTRATION NUMBER: 34,857 (Lamucci)

REGISTRATION NUMBER: 98,579 (Ranucci)

REFERENCE/DOCKET NUMBER: NA-1096D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Natick
STATE: Massa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 GDLKNKVAQLKRKVRSLKDKAAELKQEVSRLENEIEDLKAKIGDLNN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lamming, John H.
NAME: Ranucci, Vincent J.
REGISTRATION NUMBER: 22,062 (Donahue)
REGISTRATION NUMBER: 34,857 (Lamming)
REGISTRATION NUMBER: 29,579 (Ranucci)
REFERENCE/DOCKET NUMBER: NA-1096D
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o. 5712366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ?E: U.S. Army Soldier Systems Command
AMSCC-CC (Patent Counsel)
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INFORMATION:
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93.6%;
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; TYPE: amino acid
; TOPOLOGY: linear
US-08-452-592B-9
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                                                         Matches
                                                                                  Query Match
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                                                                         Best
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                             TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tirrell, David A.
APPLICANT: Kevin P. McGrath
TITLE OF INVENTION: REVERSIBLE HYDROGELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
LENGTH: 42 amino TYPE: amino acid
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                                                                                                                                                                                                                                     TELEPHONE: 61//542-8906
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ZIP: 02110-2804
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                                                                        Local Similarity
                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                          linear
                                                                                                                                           peptide
                                                                      52.8%;
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                                                       Score 199; DB 3; ...
Pred. No. 3.8e-15;
Pred-matches 0;
                                                                                                                                                                                                                                                                                           07880/033001
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Pred. No. 1.9e-15;
                                                                                    Length 42;
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                                                          Indels
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                                                         Gaps
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US-08-452-592B-6
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Best Local Similarity
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Patent No.
                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS 6.22
OPERATING SYSTEM: DOS 6.22
SOFTWARE: WordPerfect Version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,592B
FILING DATE: 25 May 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: IBM PC Compai
                                                                                                 NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. Army Soldier Systems Command
                                                                                                                                                             APPLICANT: McGrath, Kevin P.
APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using
TITLE OF INVENTION: Self-Assembling Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/068,948 FILING DATE: 25 May 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS: Army Soldier Systems Command
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using
TITLE OF INVENTION: Self-Assembling Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 508-233-4510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   16 GDLKNKVAQLKRKVRSLKDKAAELKQEVSRLENEIEDLKAKIGDLNN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Natick
STATE: Massachsuetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Donahue, Richard J.

NAME: Lamming, John H.

NAME: Ranucci, Vincent J.

REGISTRATION NUMBER: 22,062 (Donahue)

REGISTRATION NUMBER: 34,857 (Lamming)

REGISTRATION NUMBER: 29,579 (Ranucci)

REFERENCE/DOCKET NUMBER: NA-1096D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 01760-5035
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                   COUNTRY:
                                      STATE: Massachsuetts
                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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5712366
Y: United States of America
01760-5035
                                                          Natick
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                                                                             AMSCC-CC (Patent Counsel)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508-233-5167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 197; DB 1;
Pred. No. 1.4e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 84;
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US-08-956-307B-1
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Patent No. 609091
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Donahue, Richard J.

NAME: Lamming, John H.

REGISTRATION UNMBER: 22,062 (
REGISTRATION NUMBER: 34,857 (
REGISTRATION NUMBER: 9,579 (
REFERENCE/DOCKET NUMBER: NA-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-233-4510
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SOFTWARE: WordPerfect Version 6.1
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 071
TELECOMMUNICATION INFORMATION:
                                                                                                         APPLICATION NUMBER: US/08/956,307B FILING DATE: 22-OCT-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                  OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/0 FILING DATE: 25 May 1993 ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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STREET: ***
STRY: Boston
MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                            FILING DATE:
                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 amino acids
                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                         225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petka, Wendy A.
Tirrell, David A.
                                                                                                                                                                                                                                          IBM Compatible
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                   07880/033001
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TELEPHONE:

617/542-5070 7/542-8906

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RESULT 10
US-08-452-592B-11
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Best Local Similarity 76.2
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: IIBM PC COMPATABLE
OPERATING SYSTEM: DOS 6.22
SOFTWARE: WORDPERFECT VERSION 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,592B
FILING DATE: 25 May 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/068,948
FILING DATE: 25 May 1993
PRIOR APPLICATION UNMBER: 08/068,948
FILING DATE: 25 May 1993
                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/08452592B Patent No. 5712366
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino ~-'
Type
Best Local Similarity 72.9
Matches 29; Conservative
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                                                                                                                                                                  TELEFAX: 508-233-5167
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-233-4510
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                            NAME: Donahue, Richard J.

NAME: Lamming, John H.

NAME: Ranucci, Vincent J.

REGISTRATION NUMBER: 22,062 (Donahue)

REGISTRATION NUMBER: 34,857 (Lamming)

REGISTRATION NUMBER: 29,579 (Ranucci)
                                                                                                                                                                                      TELEPHONE: 508-233-5167
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States of America ZIP: 01760-5035
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STATE: Massachsuetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                LENGTH:
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                                                                                                                                 amino acid
                                                                                                                                                42 amino acids
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76.28;
               32.9%;
72.5%;
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                 Score 124; DB 1; Pred. No. 4.2e-07;
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Mismatches
                                 Length 42;
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                                                                                                                                                   Sequence 3, Application US/08956307B Patent No. 6090911
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAME: Fasse, J. Peter NAME: Fasse, J. Peter 32,983 REGISTRATION NUMBER: 0786 REFERENCE/DOCKET NUMBER: 0786 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070 TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                           TITLE OF INVENTION:
                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Fasse, J. Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 22-OCT-1997 PRIOR APPLICATION DATA:
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STREET:
CITY: I
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STATE: MA
                                                                                                                                                                                                                                                                57 IGDLNNTSGIRRPAAKLN 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
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                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRY: USA
02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                      Tirrell, David A.
Kevin P. McGrath
REVERSIBLE HYDROGELS
                                                                                                                                                                                                                                                                                                                                                                                                                                              18 amino acids
              225 Franklin Street
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Tirrell, David A.
Kevin P. McGrath
VENTION: REVERSIBLE HYDROGELS
                                                                                                                        Petka,
                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                              Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                   peptide
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100.0%;
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; Pred. No.
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                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                         DB 3;
0.00054
                                                                                                                                                                                                                                                                                                                                      Length 18
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COMPUTER READABLE FORM:

02110-2804 ĕ

USA

COUNTRY:

MEDIUM TYPE: Diskette

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; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-08-956-307B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-434-705B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/08434705B Patent No. 5798258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                TELEFAX: (206) 224-07: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BM PC COMPATIBLE
COMPUTER: PS COMPATIBLE
COMPUTER: PS COMPATIBLE
COMPATIBLE
COMPATIBLE
COMPATIBLE
COMPATIBLE
COMPATIBLE
APPLICATION DATA:
APPLICATION NAMBER: US/08/434,705B
FILING DATE: May 4, 1995
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CART PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 22-OCT-1997 PRIOR APPLICATION DATA:
                                                              ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: OH:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                 STREET: 1420 Firth CITY: Seattle STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                    ZIP: 98101
                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                         1420 Fifth Avenue, Suite 2800
                                                                                                                                                                                                                                                                                                                                      USA
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                                                   (206)
                                  224-0779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.1%;
                                                   682-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CART PROTEIN AND DNA ENCODING THEREFOR
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Pred. No.
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                                                                                            ; MOLECULE TYPE: protein
; DESCRIPTION: pET15b-r
; HYPOTHETICAL: YES
US-09-086-201-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-086-201-15
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Query Match
Best Local Similarity
Whiches 20; Conserve
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Best Local Similarity
                                                                                                                                                                                                                  TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Douglass Ph.D., James
TITLE OF INVENTION: CART PROTEIN AND DNA ENCODING THEREFOR NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                               NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: OH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/434,705
FILING DATE: May 4, 1995
ATTORNEY, AGENT INFORMATION:
NAME: Shelton, Dennis K.
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1420 F
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 K 61
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                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGSSHHHHHHSSGLVPRGSHMQEDAELQPRALDIYSAVDDASHEKELIEALQEVLKKLKS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
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5969103
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1420 Fifth Avenue, Suite 2800
                                                                                                                                                                                                        110 amino acids
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              21.9%; Score 82.5; DB 2; 32.8%; Pred. No. 0.037; tive 13; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                               us/09/086,201
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Conservative

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Search completed: July 3, 2001, 14:56:47 Job time: 537 sec
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US-08-578-649-14
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                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
                                                     Ouery Match 21.8
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                  APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Keluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                              61 K 61
                                                                                                                                                                                                                                                                                                                                                                                         56 K 56
                             21.8%;
                                                     Score 82; DB 1; Length 18; Pred. No. 0.005; Indels
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
and is derived by analysis of the total score distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
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length: 2000000000
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  July 3, 2001, 14:59:46 ; Search time 63.58 Seconds (without alignments) 88.659 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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377
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRGSHHHHHHGSMASGDLKN...
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20.4	20.4	20.4	20.6	20.6	20.6	20.7	20.7	20.7	20.7	20.8	20.8	20:8	21.0	21.0	21.0
1046	338	292	1556	778	348	1938	1313	1169	456	1956	565	564	554	407	369
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T42720	138587	151171	F96587	T30430	T04618	A40997	A48467	A64505	E86903	T16416	HMIVE2	HMIVF2	G72361	F72343	TVFVAF
cytoplasmic linker	retrovirus-related	transcription fact	hypothetical prote	hypothetical prote	heat shock protein	myosin heavy chain	myosin heavy chain		hypothetical prote	hypothetical prote	hemagglutinin prec	hemagglutinin prec	hypothetical prote	hypothetical prote	transforming prote

ALIGNMENTS

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Caccession: G69708; JC4819; PC4029
R;Kunst, F:; Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G:; Azevedo, V.; Ber
C:; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Fooliger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A;Authors: Lanber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddie, Y.; Sato, T.; Scani
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sea
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Zumstein, E.; Yoshikawa, H.; Sachikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A;Reference number: A69580; MUID:98044033 chromosome segregation SMC protein - Bacillus subtilis N;Alternate names: minichromosome stabilizing protein : C:Species: Bacillus subtilis

A; Accession: G69708 A; Status: nucleic a acid sequence not shown; translation not shown

R:Oguro, A.; Kakeshita, H.; Takamatsu, H.; Nakamura, K.; Yamane, K.
Gene 172, 17-24, 1996
A;Title: The effect of Srb, a homologue of the mammalian SRP receptor alpha-subunit, A;Reference number: JC4819; MUID:96257247
A;Recession: JC4819 A;Molecule type: DNA A;Restdues: 1-1186 <KUN> A;COSS-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13467.1; PID:g26339 A;Experimental source: strain 168

A;Molecule type: DNA A;Restidues: 1-49,'G',51-161,'G',163-174,'E',176-177,'G',179-191,'G',193-227,'P',229-2 74,'P',476-493,'D',495-514,'D',516-541,'V',543-545,'P',547-585,'SKPLRGNSGPAFIISF',601

A;Cross-references: DDBJ:D64116; NID:g1389548; PIDN:BAA10977.1; PID:g1237015
R;Oguro, A.; Kakeshita, H.; Honda, K.; Takamatsu, H.; Nakamura, K.; Yamane, K.
DNA Res. 2, 95-100, 1995
A;Title: srb: a Bacillus subtilis gene encoding a homologue of the alpha-subunit of A;Reference number: JC4093; MUID:96093930

A; Accession: PC4029

A;Molecule type: DNA A;Residues: 1171-1186 <0G2> A;Cross-references: DDBJ:D49781; NID:g1237017; PIDN:BAA08615.1; PID:g1237018

chromosome segregation protein SMC1

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C;Geneti
A;Gene:
C;Superf
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Somite Maf1 protein - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Species: " "~~-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                        Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666
A;Accession: A70359
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
A70359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: DDBJ:AB006324
C;Comment: This protein, a member of
mportant roles in somitogenesis, and
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S
                                                                                                                                                            A;Cross-references: GB:AE000701; NID:g2983260; PIDN:AAC06860.1; PID:g2983266; GB:AE00065
A;Experimental source: strain VF5
                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-259 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                      hydrogenase expression/formation protein B - Aquifex aeolicus
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                                                                                                                                                                                                                                                                                                                          R;Deckert, G.; Warren, P.V.; Gaasterland, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-315 <KAJ>
                                                                                                                                                                                                                                                                                                                                       ;Species: Aquifex aeolicus
;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 24-Sep-1999
;Accession: A70359
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Best Local Similarity 36.8
                                                                                                             ;Superfamily: hydrogenase expression/formation protein hypB
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                                               Query Match
Best Local
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Best Local Similarity
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 HHHHHHGSMASGDLKNKVAQLKRKVRSLKDKAAELKQ-----
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26; Conser
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                                               23.3%;
                                 12;
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                               Score 88; DB
Pred. No. 1.7;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 89; DB 3; Pred. No. 1.7;
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1.7;
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                                                               Length 259
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RESULT 4
ISO167
B-G antigen - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Kaufman, J.; Salomonsen, J.; Skjoedt, K. Immunogenetics 30, 440-451, 1989
A; Title: B-G clones have multiple small repeats A; Reference number: I50161; MUID: 90077532
A; Accession: I50167
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-323 <RES>
A;Cross-references: GB:L36435; NID:g625043; PIDN:AAA65689.1; PID:g625044
A;Cross-references: GB:L36435; NID:g625043; PIDN:AAA65689.1; PID:g625044
C;Superfamily: maf transforming protein; maf homology
C;Keywords: leucine zipper; transcription factor
F;212-301/Domain: maf homology <MAF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Cordes, S.P.; Barsh, G.S.
Cell 79 (1025-1034, 1994
A;Title: The mouse segmentation gene kr encodes
A;Reference number: A55200; MUID:95094266
A;Accession: 149529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription factor-kr - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1996 #sequence_revision
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I49529
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A; Residues: 1-155 <KAU>
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Best Local
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 282
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                                   41 QEVSRLENEIEDLKAKIGDLNNTSGIR 67
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                                                                       RELNRHLRGFTKDEVIRLKQKRRTLKNRGYAQSCRYKRVQQKHHLENEKTQLIQQVEQLK
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                                                                                               -GDLKNKVAQLKRKVRSLKDK--
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23.1%;
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Pred. No. 1.5;
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Pred. No. 3.4;
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 307
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C:Species: Mycoplasma hyorhinis
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993
C:Accession: JQ0894
R:Notarnicola, S.M.; McIntosh, M.A.; Wise, K.S.
Gene 97, 77-85, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Gallus gallus (chicken)
C;Species: 20-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 21-Jul-2000
C;Accession: D39371
R;Miller, M.M.; Goto, R.; Young, S.; Chirivella, J.; Hawke, D.; Miyada, C.G.
Proc. Natl. Acad. Sci. U.S.A. 88, 4377-4381, 1991
A;Title: Immunoglobulin variable-region-like domains of diverse sequence within the major A;Accession: D39371
A;Accession: D39371
A;Status: preliminary
Gene 97, 77-85, 1991
A;Title: A Mycoplama hyorhinis protein with sequence similarities
A;Reference number: JQ0894; MUID:91138990
A;Accession: JQ0894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein PAB0812 - Pyrococcus abyssi (strain Orsay) C;Species: Pyrococcus abyssi C;Chate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 02-Feb-200C;Accession: F75103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: PAB081;
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-880 <KAW>
A;Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence:
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A; Accession: F75103
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A; Residues: 1-321 <MIL>
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Best Local S
Matches 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLAEKDLSTADLKLLAAKLVEQREAVEERDSQLRKQYEKLGSRATNLKTQLKKLENEIEE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKAKIGDLNNTSGIRRPAAKLN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HHHHGSMASGDLK------NKVAQLKRKVRSLKDKAAELKQEVSRLENEIED 52
                                                                                                                                                                                                                                                                                                                                                        Similarity 37.:
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaeoglobus fulgidus
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                                                                                                                                                                                                                                                                                                                                                                           22.5%;
37.2%;
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26.8%;
                                                                                                                                                                                                                                                                                                                                                        14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262
                                                                                                                                                                                                                                                                                                                                                      Score 85; DB
Pred. No. 10;
L4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 85;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insights
                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #text_change 02-Feb-2001
                                                                                                                         #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                             Length 880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 321
                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:CAB50131.1; PID:g54586
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                                           nucleotide-binding
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A; Molecule type: DNA
A; Residues: 1-979 <NOT>
A; Cross-references: GB:M34956
A; Cross-references: GB:m34ed the cc.; Comment: This protein is located in C; Genetics:
A; Genetics:
A; Genetic code: SGC3
                                                                                                                                               R;Geisel, C.; Bradshaw, H.; Wamsley, P. submitted to the EMEL Data Library, Novemb A;Description: The sequence of C. elegans A;Reference number: 220578
A;Accession: T29145
                                                                                                                                                                                                                                                               hypothetical protein F56A3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-281 <KAW>
A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49181.1; PID:g545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999
C:Accession: F75216
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C;Keywords: nucleotide binding; P-loop
F;32-39/Region: nucleotide-binding motif A (P-loop
                                                       A; Cross-references: EMBL: U80446; PIDN: AAB37802.1; A; Experimental source: strain Bristol N2; clone F
                                                                                         A; Molecule type: DNA
A; Residues: 1-1199 <GEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
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A; Accession: F75216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999
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A; Map position:
                 A;Gene:
                                                   A; Experimental source: strain
                                                                                                                           A; Status: preliminary; translated
                                                                                                                                                                                                                                             C; Accession: T29145
                                                                                                                                                                                                                                                                                                                            T29145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain Orsay
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Best Local Similarity
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Best Local Similarity
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                 CESP: F56A3.4
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 84.5;
Pred. No. 3
                                                                                                                                 from GB/EMBL/DDBJ
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                                                     clone F56A3
                                                                                                                                                                                       cosmid F56A3
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                                                                         GSPDB:GN00019; CESP:F56A3.4
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R:Yuasa, H.J.; Sato, S.; Yamamoto, H.; Takagi, T.
J. Biochem. 122, 374-380, 1997
A;Title: Primary structure of troponin I isoforms
A;Reference number: JC5610; MUID:98021076
A;Accession: JC5610
                                                                                                                                                                                                                                                                                                                                                                                                        R:Kataoka, K.; Fujiwara, K.T.; Noda, M.; Nishizawa, M. Mol. Cell. Biol. 14, 7581-7591, 1994
A;Title: MafB, a new Maf family transcription activator A;Reference number: A56235; MUID:95021288
A;Accession: A56235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Gallus gallus (chicken)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 20-Jun-2000
C:Accession: A56235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: DDBJ:AB001685; NID:g1888344; PIDN:BAA19425.1; PID:g1888345 A;Experimental source: adult Halocynthia roretti C;Comment: This protein binds to actin, and inhibits the interaction between actin and C;Superfamily: troponin I
                                                                                                                                                                                                                                        A;Introns: #status absent
C;Superfamily: maf transforming protein; maf homology
C;Keywords: DNA binding; homodimer; leucine zipper
C;Keywords: DNA binding; homodimer; leucine zipper
F;200-289/Domain: maf homology <MAF>
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A; Residues: 1-311 <KAT>
A; Cross-references: GB:D28600; NID:g516723; PIDN:BAA05938.1; PID:g516724
                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcription activator MafB - chicken
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A; Residues: 1-173 <YUA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 18/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roponin I - sea squirt (Halocynthia roretzi);Species: Halocynthia roretzi
;Species: Halocynthia roretzi
;Date: 23-Sep-1997 #sequence_revision 17-Oct-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: JC5610
                                                                                                                                                                 Query Match
Best Local Similarity
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Best Local 9
                                                                                                                                                  Matches
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     219
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les 18; Conserv
                                      17 DLKNKVAQLKRKVRSLKDK----
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                                                                                                                                                Conservative
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                                                                                                                                                                 21.8%; Score 82;
21.7%; Pred. No.
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Pred. No. 3.5;
16; Mismatches
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Pred. No. 16;
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                                      ---AAELKQEVSRLENE 49
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                    chromosome segregation SMC protein smc [imported] - Bacillus halodurans (strain C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000 C;Accession: G83960
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C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 29-Oct-1999
C;Accession: S37894; S37897; S39170; S44515
R;Rasmussen, S.; von Wettstein, D.
submitted to the Protein Sequence Database, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data A; Reference number: S39168 A; Accession: S39170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; ACCESSION. A; MOLECULE type: DNA
A; Molecule type: DNA
A; Residues: 1-557 <POH>
A; Cross-references: EMBL: Z28072; MIPS: YKL072w
A; Cross-references: Strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast 10, 69-74, 1994
A;Title: Sequence of a 20.7 kb region of yeast chromosome XI includes the NUP100 gene rp in addition to seven ORFs with weak or no significant similarity to known proteins A;Reference number: S44513
A;Reference number: S44515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S37897
A; Accession: S37897
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A; Accession: S37894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EME
A;Note: the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-766 < RA3>
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A; Residues: 1-766 <RA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain R; Pohl, T.M.; Pohl, F.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z28072; NID:g486100; A;Experimental source: strain S288C
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A; Residues: 1-766 < RAS>
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                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 20; Conserv
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083
                                                     52 DLKAKIGDLNNTSGI 66
                                                                                                                                                         2 RGSHHHH-HHGSMAS----
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DVRKKLLEQNNSKDI 694
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lde sequence was submitted to the EMBL Data Library, November 1993
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26.7%;
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Pred. No. 15;
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Nakasone, K.;

Takaki,

Y.;

Maeno,

G.;

Sasaki,

R.; Masui, N.; Fuji,

C-125

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hypothetical protein AF1225 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: H69402
R;KLenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Accession: H69402
A;Cocssion: H69402
A;Cocssion: H69402
A;Cocssion: Poliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-212 (KLE)
A;Cocssion: H69402
A;Residues: 1-212 (KLE)
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20263314
A;Accession: G83960
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1188 <STO>
A;Cross*references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06206.1; GSPDB:GN00A;Experimental source: strain C-125
C;Genetics:
G;Genetics: smc
Search completed: July Job time: 372 sec
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Perfect score:
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Kuboki Y., Nishizawa M., Nishi S.;
"Rat maf related genes: specific expression in chondrocytes,
spinal cord.";
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1- SUBCELLULAR LOCATION: NUCLEAR.
1- SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
SEQUENCE FROM N.A. Izard J., Chartier M., Baty Submitted (MAY-1995) to the -!- FUNCTION: THIS COLICIN
                                                                     MEDLINE-96074330; PubMed-
Pilsl H., Braun V.;
"Strong function-related
and 5.";
                                                                                                                                                                                                                          COLICIN K
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DOMAIN
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                                                                                                                    STRAIN-K49
                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                    Escherichia
                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                       Escherichia coli.
Plasmid Colk-K235
                                                                                                                                                                                                                                                                                                                                               282
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                                                          Bacteriol. 177:6973-6977(1995)
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                                                                                                                                                                                                                                                                                                                                              QEVSRLARERDAYKVKCEKLAN-SGFR 307
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                                                                                                        PubMed=7592493;
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167
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Last annotation update)
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ICIN IS A CHANNEL-FORMING
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POLY-HIS.
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LEUCINE-ZIPPER.
6E386340D1F840A5
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                                                                                                                                                                              subdivision; Enterobacteriaceae;
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L outstation -
  CLASS
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Best Local Similarity 32.1
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _MOUSE
MAF1_MOUSE
P54841;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstarion the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                 zipper transcription factor.";
Cell 79:1025-1034(1994).
-1- FUNCTION: MAY PLAY AN EARLY ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
TRANSCRIPTION FACTOR MAF1 (SEGMENTATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00280; CHANNEL_COLICIN; PROSITE; PS00276; CHANNEL_COLICIN; PARTISHED S05 155 POTENT S05 155 S -> C
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-I- FUNCTION: COLICINS ARE POLYPEPTIDE TOXINS PRODUCED BY AND ACTIVE AGAINST, ESCHERICHIA COLI AND CLOSELY RELATED BACTERIA.

-I- SIMILARITY: BELONGS TO THE CHANNEL FORMING COLICIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X87834; CAA61099.1; -. EMBL; U27452; AAB41288.1; -.
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or send
                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                        Cordes S.P., Barsh G.
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95094266; PubMed=8001130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAFB OR MAF1 OR KRML.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                     SUBCELLULAR LOCATION: NUCLEAR.

TISSUE SPECIFICITY: MOST ABUNDANT IN KIDNEY, GUT, LUNG, AND BRAIL DEVELOPMENTAL STAGE: DETECTABLE AT 8.0 DPC (ONE SOMITE) AS A BANI IN THE CAUDAL HINDBRAIN, AND BY 8.5 DPC (SIX TO EIGHT SOMITES), THE HIGH LEVEL DOMAIN EXHIBITS A SHARP ROSTRAL EDGE COINCIDENT WITH THE R4/R5 BOUNDARY AND A DIFFUSE CAUDAL EDGE LOCATED MIDWAY THROUGH R6.
                                                                                                                                      SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                   SEGMENTATION).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HHHHHGSMASGDLKNKVAQLKRKVRSLKDKAAELKQEVSRLENEIEDLKAKIGDLN 61
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an
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59661 MW;
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Rodentia;
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Pred. No. 1.8;
13; Mismatches
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Sciurognathi; Muridae;
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01-FEB-1996
15-JUL-1998
                                                                                                                                                                                                  PIR; JQ0894;
ATP-binding;
                                                                                                                                                                                                                                                                                                                                       or send
                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 97:77-85(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=91138990; PubMed=1825306;
Notarrnicola S.M., McIntosh M.A., Wise K.S.;
"A Mycoplasma hyorhinis protein with sequence similarities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma hyorhinis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Mycoplasmataceae; Mycoplasma.
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HSSP; P05412; LJUN.
                                                                                                                                                                                                                                                                   EMBL; M34956; AAA25423.1;
                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide-binding enzymes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 QEVSRLENEIEDLKAKIGDLNNTSGIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
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(Rel. 33, Last sequence up)
(Rel. 36, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                JQ0894.
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Pred. No. 1.
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LEUCINE-ZIPPER.
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SEQUENCE

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RESULT 6
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                                                                                                                                            EMBL; X75780; CAA53402.1; -.
EMBL; Z28072; CAA81909.1; -.
PIR; S37894; S37894.
PIR; S39170; S39170.
PIR; S44515; S44515.
SGD; S0001555; YKL072W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STB6_YEAST
P36085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of the Saccharomyces encoding Sin3p binding proteins."; Mol. Gen. Genet. 256:376-386(1997).
-i- FUNCTION: BINDS TO SIN3.
                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-557 FROM Pohl T.M., Pohl F.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence of a 20.7 kb region of yeast chromosome XI includes the NUP100 gene, an open reading frame (ORF) possibly representing a nucleoside diphosphate kinase gene, tRNAs for His, Val and Trp in addition to seven ORFs with weak or no significant similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales;
NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STB6 PROTEIN.
STB6 OR YKL072W OR YKL352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994
01-OCT-2000
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                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kasten M.M., Stillman D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98055153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rasmussen S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94378724; PubMed-8091863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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10:S69-S74(1994).
  Similarity
20; Conser
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(Rel.)
21.8%;
llarity 26.7%;
Conservative ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=9393435;
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40,
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Score 82; DB
Pred. No. 5.5;
0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                          9BCBEA2EE03A9AF1 CRC64;
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Տ
                                              Length 766;
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RESULT 8
Y334_M
ID Y334_M
AC Q57780
DT 01-NOV
DT 01-NOV
DT 01-NOV
DE HYPOTH
GN MAJ0334
OS Methan
OC Archae
OC Methan
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YB38_MYCPN
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Best Local S
Matches 16
                                                                                           Y334_METJA
Q57780;
Q1-NOV-1997 ()
Q1-NOV-1997 ()
Q1-NOV-1997 ()
HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YB38_MYCPN
P75260;
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002862; -. Pfam; PF01519; DUF16; 1. Hypothetical protein. SEQUENCE 166 AA; 19518
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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01-OCT-2000 (Rel. 40, Last a
HYPOTHETICAL PROTEIN MPN138
MPN138 OR MP016.
 SEQUENCE FROM N.A
                          Methanococcus.
NCBI_TaxID=2190;
                                                                 Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 24:4420-4449(1996).
-!- SIMILARITY: BELONGS TO THE UPF0134 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Hinmelreich R., Hilbert H., Plagens H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000
                                                     Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000003; AAB95664.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2104;
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(Rel.
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Last annotation updat
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                                                      Methanococcales; Methanococcaceae;
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Pred. No.
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RESULT 9
SMC1_YEAST
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Best Local
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Saccharomyces cerevisiae.";
Saccharomyces cerevisiae.";
Nat. Genet. 10:261-268(1995).
-I- FUNCTION: INVOLVED IN CHROMOSOME SEGREGATION IN MITOSIS.
-I- FUNCTION: OF A CHROMOSOME CONDENSATION MOTOR.
-I- SUBUNIT: HOMODIMER OR HETERODIMER WITH-SMC2 OR OLIGOMERS
-I- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus lannaschii.";
                                                                                                                                  Murakami Y., Naitou M., Hagiwara H., Shibata T.,
Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda
Yamazaki M., Tashiro H., Eki T.;
                                                                                                                                                                                                                                                                                        MEDIANCE 4103320; PubMed-8276886;
Strunnikov A.V., Larionov V.L., Koshland
"SMC1: an essential yeast gene encoding a
protein is required for nuclear division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-yUL-1998 (Rel. 36, Last annotation update
CHROMOSOME SEGREGATION PROTEIN SMC1 (DA-BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                         protein is required for nuclear d:
protein family.";
J. Cell Biol. 123:1635-1648(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMC1_YEAST
P32908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                             Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence
                                                                                                                                                                                     STRAIN=S288C / AB972;
MEDLINE=95400292; PubMed=7670463;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 273:1058-1073(1996).
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MJ0334; -.
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Pred. No. 0.96;
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            entities
or send a
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                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not remove
entities requires a license agreement (So
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS -i- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                -1- FUNCTION: HEMAGGIUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-1- SUBBUNIT: HOMOTRIMER. EACH OF THE MONMER IS FORMED BY TWO CHAINS (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
                                                                                                                                                                                                             Kawaoka Y., Bean W.J., Webster R.G.;
"Evolution of the hemagglutinin of equine H3 influenza viruses.";
Virology 169:283-292(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitosis;
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PIR; S41804; S41804.
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-89204899; PubMed=2705299;
                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA negative-strand
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                                                                                                                                    - !- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11393;
                                                                                                                                                                                                                                                                                                                       Influenza A virus.
                                                                                                                                                                                                                                                                                                                                    Influenza virus A and
                                                                                                                                                                                                                                                                                                                                                      Influenza A virus (strain A/Equine/Algiers/72).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                             HEMAGGLUTININ HA2 CHAIN]
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D50617; BAA09230.1;
D31600; BAA06496.1;
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19; Conservative
            requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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COILED COIL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL ()
ALA/ASP-RICH (DA-BOX).
S-Y-L: IN TS MUTANT SMC1-2.
N-D): IN TS MUTANT SMC1-1.
MW; B504017AA0ECCA8C CRC64;
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Pred. No.
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Best Local
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SIGNAL 1
CHAIN 17
CHAIN 345
CARBOHYD 23
CARBOHYD 37
CARBOHYD 53
CARBOHYD 78
CARBOHYD 180
CARBOHYD 300
CARBOHYD 498
SEQUENCE 565 AA;
                                                                                                                                                    MEDLINE-89204899; PubMed-2705299;
KRAWACKA Y., Bean W.J., Webster R.G.;
KRAWACKA Y., Bean W.J., Webster R.G.;
KRAWACKA Y., Bean W.J., Webster R.G.;
POLITION of the hemagglutinin of equine H3 influenza vi
Virology 169:283-292(1989).

-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING
CELL RECEPTORS AND FOR INITIATING INFECTION.

-I- SUBUNIT: HOMORINER. EACH OF THE MONOMER IS FORMED BY
(HAI AND HA2) LINKED BY A DISULFIDE BOND.
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                                                                                                                                                                                                                                                                                                                                                                                     HEMA_IAHTO STANDARD; PRT; 565 AA.
P17000; Q84002; Q84003;
01-AUG-1990 (Rel. 15, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HAZ CHAIN].
                                                                                                                                                                                                                                                                                                                            Influenza A virus (strain A/Equine/Tokyo/71).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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Influenza A virus.
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                                                                                                                                        SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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63831 MW;
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AAA43111.1; ALT_SEQ
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28.1%;
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HEMAGGLUTININ HA2 CH
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 79.5; DB Pred. No. 6.5; L5; Mismatches
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EMBL; M26769; AAA42377.1;
PIR; B33975; TVFVAF.
HSSP; P05412; 1JUN.
                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                the
                                                                                                                                                                                                                                                                        MEDLINE=90046665; pubMed=2554284;
Nishlawa M., Kataoka K., Goto N., Fujiwara K.T., Kawai Sushilawa M., Kataoka K., Goto N., Fujiwara K.T., Kawai Sushilawa M., Kataoka K., Goto N., Fujiwara K.T., Kawai Sushilawa M., Kataoka K., Goto N., Fujiwara K.T., Kawai Sushilawa M., Kataoka K., Goto N., Fujiwara K., Kawai Sushilawa M., Kataoka M., Kataoka M., Fujiwara M., Kataoka M., Fujiwara K., Fujiwara K., Kawai Sushilawa M., Fujiwara K.T., Kawai Sushilawa M., Fujiwa M., Fu
                                                                                                                                                                                                                                                                                                                                                                                                                                      Avian musculoaponeurotic fibrosarcoma virus AS42. Viruses; Retroid viruses; Retroviridae; Avian typ NCBI_TaxID-11873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00329; PRINTS; PR00330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00509; Hemagglutinin; PRINTS; PR00329; HEMAGGLUTN12
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HSSP; P03437;
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                                                                         send an email to license@isb-sib.ch).
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                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                       MISCELLANEOUS: THIS
                                                                                                                                                                                                                                        POLYPROTEIN.
                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                        license agreement (See http://www.isb-sib
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HEMAGGLUTININ HA2
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RESULT 13
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DOMAIN
                      Pfam; PF00509; Hemagglutinin; PRINTS; PR00339; HEMAGGLUTN12. PRINTS; PR00330; HEMAGGLUTN1. PRINTS; PR00331; HEMAGGLUTN2.
                                                                                                                     InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          different regions of the world.";
Virology 169:408-417(1999).
1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
CELL RECEPTORS AND FOR INITIATING INFECTION.
1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO CHAIN
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                           EMBL; M25284; AAA43217.1;
PIR; B34214; HMIVF2.
HSSP; P03437; 2HMG.
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01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-89204912; PubMed-2705304;

Donis R.O. Bean W.J., Kawaoka Y., Webster R.G.;

"Distinct lineages of influenza virus H4 hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Influenza A virus (strain A/Grey teal/Australia/2/79).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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17, Last sequence update)
39, Last annotation update
  Hemagglutinin; Glycoprotein; Signal
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LEUCINE-ZIPPER
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RESULT 14
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Best Local
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"Amino acid sequences of haemagglutinins of influenza viruses c
"Amino acid sequences of haemagglutinins of influenza viruses c
"H3 subtype isolated from horses.";

J. Gen. Virol. 66:457-464(1985).

-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VI
CELL RECEPTORS AND FOR INITIATING INFECTION.

-I- SUBJULT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO C
(HAI AND HA2) LINKED BY A DISULFIDE BOND.

-I- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CARBOHYD
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                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               Kawaoka Y., Bean W.J., Webster R.G.; "Evolution of the hemagglutinin of e Virology 169:283-292(1989).
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Influenza virus A and B group;
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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HEMAGGLUTININ HA2 CHAIN.
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EMBL; M24719; AAA43105.1; EMBL; M29257; AAA43164.1; PIR; B34064; HMIVE2. HSSP; P03437; 1HTM.

ALT_SEQ

InterPro;

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RESULT 15
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Best Local S
Matches 17
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P24733;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN, STRIATED MUSCLE.
Aequipecten irradians (Bay scallop).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
Pectinoidea; Pectinidae; Argopecten.
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PRINTS; PR00330; HEMAGGLUTN1.
PRINTS; PR00331; HEMAGGLUTN2.
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                                                                                                                         TISSUE-Adductor muscle; MEDLINE-91088319; PubMe
                                                                                                                                                                                                TISSUE-Adductor muscle;
MEDLINE-92011595; PubMed-1917970;
MYILINE-92011595; PubMed-1917970;
NyiLray L., Goodwin E.B., Szent-Gyoergyi A.G.;
"Complete primary structure of a scallop striated muscle myosin heavy chain. Sequence comparison with other heavy chains reveals regions that might be critical for regulation.";
T. Biol. Chem. 266:18469-18476(1991).
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x-ray CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 777-836 MEDLINE-94173332; PubMed-8127365;
                                                  Nyitray L., Goodwin E.B., Szent-Gyorg
"Nucleotide sequence of full length c
muscle myosin heavy chain.";
Nucleic Acids Res. 18:7158-7158(1990)
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-31199;
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JR PKINTS; PROUSES, MACHINES, PROSTEE; PESO096; IO; 1.

W Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; W Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; W Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; W Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; W Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; W Myosin; W Myosin; W Myosin; W Myosin; Muscle protein; Schollar Filed Coiled Coil; Thick filament; Actin-binding; W Myosin; W Myosin; W Myosin; Muscle pattern; 3D-structure.

ET DOMAIN 836 1938 COILED COIL (POTENTIAL).

ET DOMAIN 778 805 IQ.

ET NOD_RES 693 693 ALKYLATION (SH-1) (BY SIMILARITY).

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InterPro; IPR002928; -.
Pfam; PP00612; IQ; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF0063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - I FUNCTION: MUSCLE CONTRACTION.
- I FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPAS ACTIVITY THAT IS ACTIVATED BY F-ACTIN.
- I SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
- I SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
- I SIMILARITY: CONTAINS 1 10 DOMAIN.
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PIR; A40997; A40997.
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O9uzc8 pyrococcus
O9v271 pyrococcus
O9v273 homo sapien
P91349 caenorhabdi
O01354 halocynthia
O90888 gallus gall
O9pua6 xenopus lae
                                                                                                                                          Q9h1f1 homo sapien
Q31620 gallus gall
Q9lax2 streptococc
Q9lax3 streptococc
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Q9w6b1 brachydanio
Q31405 gallus gall
O42290 gallus gall
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O73679 brachydanio
Q91891 gallus gall
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xenopus lae
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Q9v7n6 drosophila	Q20641 caenorhabdi		Q9lay5 streptococc	Q9wzh0 thermotoga	Q92171 gallus gall	Q9vuk4 drosophila	Q91xr8 arabidopsis	Q9igsO influenza a	Q02456 schistosoma	Q9u679 strongyloce	Q26589 schistosoma	Q90370 coturnix co	Q9hqm8 halobacteri	054615 legionella	Q9u7e3 pecten maxi	096398 schistosoma		Q9yac7 aeropyrum p	~		O	Q9mc79 bacteriopha		Q9ka07 bacillus ha	Q9lax6 streptococc

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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF07/1821; AAF27/16.1; -.
Interpro; IPR002965; -.
PRINTS; PR01217; PRICHEXTENSN.
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Hollingshead S.K., Becker R., Briles D.E.;
"Diversity of PspA: mosaic genes and evidence for past recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                          17 DLKNKVAQLKRKVRSLKDKAAELKQEVSRLENEIEDLKAKIGD 59
:|:||| | |:::: | |:|::|| ::| |:
215 ELQNKVADLEKEIADVKKTVADLEKEVAKLEKDVEGFKESDGE 257
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(TremBLrel. 07, Created)
(TremBLrel. 07, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.18;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 91; DB 2;
Pred. No. 3.1;
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                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 481;
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                                                                       Matches
                                                                                              Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91891; Q91891891; Q91891; Q91891; Q91891; Q91891; Q91891; Q91891; Q91891; Q91
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EMBL; AF000641; AAC18821.1; -.

ZFIN; ZDB-GENE-980526-515; val.

InterPro; IPR001871; -.

SMART; SM00338; BRLZ; 1.

SEQUENCE 356 AA; 40243 MW; 07
                                                                                                                                                                                                                          NON_TER
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MEDLINE-98165393; PubMed-9425134;
Moens C.B., Cordes S.P., Glorgianni
Moens C.B., Cordes S.P., Glorgianni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-2000) to the EMBL; AF221558; AAF71240.1; EMBL; AF221557; AAF71239.1; InterPro; IPR001871;
                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                             specific genes."
Submitted (JAN-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BREED FAYOUMI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-7955,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VALENTINO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genetic variation among chicken lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Equivalence in the genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTSGIR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRTLKNRGYAQSCRFKRVQQKHLLENEKTQLINQVEQLKQEINRLARERDAYKLKCEKLT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRSLKDK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HHHHHHPHGHPGQQGHHGVGGGLNVEDRFSDDQLVTMSVRELNRHLRGFTKDEVIRLKQK 274
         SHHHHHHG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               НННННН----
                                                                                                                                                                                                                                                                                                                     SM00338; BRLZ; 1.
                                                                    28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lamont S.J.;
                                                                                                                                                                                                                          146
146 AA;
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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17579
                                                                                           23.5%;
27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND BREED G-B1
                                                                                                                                                                                                                             ME.
         -SMASGDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
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                                                                 Score 88.5; D
Pred. No. 1.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 89.5; Di
Pred. No. 3.1;
                                                                                                                                                                                                                             382BAD1D098E1DCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEGHORN; TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---AAELKQEVSRLENEIEDLKAKIGDLN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
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6
   -KNKVAQLKRKVRSLKDK-----
                                                                                                                               DΒ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mammalian species
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; Ostariophysi;
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Best Local S
Matches 28
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NCBT m-
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066901;
01-AUG-1998
InterPro; IPR002894; -.
InterPro; IPR002894; -.
Pfam; PF01495; HypB_UreG; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2; UNKNOWN_1.
PROSITE; PS00028; ZINC_FINGER_C4528C8CFA53806C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       057342 PRELIMINARY; PRI
057342;
01-JUN-1998 (TrEMBLrel. 06, Creat
01-JUN-1998 (TrEMBLrel. 06, Last
01-MAR-2001 (TrEMBLrel. 16, Last
                                                                                                                                                                                                                                                                              Deckert G., Warren P.V., Gaasterland T
Graham D.E., Overbeek R., Snead M.A.,
Feldman R.A., Short J.M., Olson G.J.,
"The complete genome of the hypertherm
aeolicus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00338; BRLZ; SEQUENCE 286 AA; 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Benkhelifa S., Felder-Schmittbuhl M.P., Calothy submitted (NOV-1997) to the EMBL/GenBank/DDBJ da EMBL; AF034693; AAC60377.1; -. Interpro; IPR001871; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                       Nature 392:353-358(1998).
EMBL; AE000701; AAC06860.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98196666; PubMed-9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYDROGENASE
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                                                                                                                                                                   InterPro; IPR000822;
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l Similarity 27.5%;
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nead M.A., Keller M., Aujay M., Hube-
lson G.J., Swanson R.V.;
hyperthermophilic bacterium Aquifex
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11; Mismatches
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"Expression of Zkrml2, a homologue of the Krml1/val segmentation during embryonic patterning of the zebrafish (Danio rerio).";

Mech. Dev. 80:223-226(1999).

EMBL; AF109781; AAD26141.1; -.

InterPro; IPR001871; -.

SMART; SM00338; BRLZ; 1.

SMART; SM00338; BRLZ; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Catinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=9031; [1]
                                                                                                                                           Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-99173794; PubMed-10072793;
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(TremBLrel. 12, Last sequence update)
(TremBLrel. 16, Last annotation update)
Tremotive Zipper Transcription Factor.
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Pred. No.
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Pred. No.
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mes; Phasianidae; Phasiani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Induction of lens differentiation by activation of a bZIP transcription factor, L-Maf."; Science 280:115-118(1998) EMBL; AF034570; AAC15781.1; -
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"B-G cDNA clones have multiple small repeats and hybridize to both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ogino H., Yasuda K.;
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RIPTION FACTOR L-MAF.
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01-NOV-1996
01-MAR-2001
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Q31620;
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submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL035665; CAB75863.1; -.
SEQUENCE 323 AA; 35792 MW; A0F3C09F8936CB16 CRC64;
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SEQUENCE
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MEDLINE-91239571; PubMed-1903541;
MILLER M.M., Goto R., Young S., Chirivella J., Hawke D., Miyada (
"Immunoglobulin variable-region-like domains of diverse sequence
within the major histocompatibility complex of the chicken.";
Proc. Natl. Acad. Sci. U.S.A. 88:4377-4381(1991).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DJ644L1.1 (KREISLER
                                                                                                                                                                                                                                                                                                                                                                    EMBL; M61862; AAA48627.1; -.
InterPro; IPR003006; -.
InterPro; IPR003600; -.
Pfam; PF00047; 1g; 1.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00410; IG_like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
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                                                                                                                                                Local Similarity 26.8 165 22; Conservative
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                                                  HLAEKDLSTADLKLLAAKLVEQREAVEERDSQLRKQYEKLGSRATNLKTQLKKLENEIEE
LKAKIGDLNNTSGIRRPAAKLN 74
                                                                                              HHHHGSMASGDLK-------NKVAQLKRKVRSLKDKAAELKQEVSRLENEIED
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                                                                                                                                                                                                                                                                        321 AA;
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Primates;
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36360 MW;
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Pred. No. 6;
9; Mismatches
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                                                                                                                                                Score 85; DB 7
Pred. No. 6.6;
18; Mismatches
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                                                                                                                                                                                                                                                                        7F25BD29E39860C7 CRC64;
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"Diversity of PspA: mosaic genes and evidence for in Streptococcus pneumoniae.";
submitted (JUN-1998) to the EMBL/GenBank/DDBJ dat EMBL; AF071826; AAF27719.1; -.
InterPro; IPR00533; -.
InterPro; IPR002965; -.
InterPro; IPR002965; -.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR0124; TROPMYOSIN.
PRINTS; PR0124; TROPMYOSIN.
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Q9LAX2;
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PSPA (FRAGMENT).
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O1-OCT-2000 (TrEMBLrel. 15,

O1-MAR-2001 (TrEMBLrel. 16,
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SEQUENCE
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                                                                                                                                 PRINTS; PR01217; PRICHEXTENSN PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                          Hollingshead S.K., Becker R., Briles "Diversity of PspA: mosaic genes and
                                                                                                                                                                                                                                                                                                                                  STRAIN-BG7561;
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NCBI_TaxID=1313;
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Best Local Similarity
Matches 16; Conserv
"Pyrococcus abyssi genome sequence: insights int structure and evolution";
structure and evolution";
submitted (JUL-1999) to the EMBL/GenBank/DDBJ da EMBL; A2248283; CAB49181.1; -.
Interpro; IPR000533; -.
Interpro; IPR002017; -.
Interpro; IPR002017; -.
PRINTS; PR00194; TROPOMYOSIN.
Hypothetical protein.
SEQUENCE 281 AA; 32744 MW; 8AA7BC80D1B5B877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Q9V217; Q9V217;
01-MAY-2000 (TrEMBLrel. 13, Cres
01-MAY-2000 (TrEMBLrel. 13, Last
01-JUN-2000 (TrEMBLrel. 14, Last
HYPOTHETICAL 32.7 KDA PROTEIN.
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InterPro; IPRO01238; -.
InterPro; IPRO01687; -.
InterPro; IPRO03439; -.
InterPro; IPRO03593; -.
Pfam; PF00470; RecF; 1.
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Q9UZC8;
Q1-MAY-2000
01-MAY-2000
01-MAR-2001
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AJ248286; CAB50131.1; .
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Archaea; Euryarchaeota;
NCBI_TaxID=29292;
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Archaea; Euryarchaeota;
NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                            STRAIN-ORSAY;
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                                                                                                                                                                                                                                                                                                                        He111g R.;
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Pred. No. 17;
14; Mismatches
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       8AA7BC80D1B5B877 CRC64;
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Q9Y5Q3;
                                                                                                                                                                                                            Wang P.W., Eisenbart J.D., Barsh G.S., Stoffel M., Le Be "Human MAFB: cDNA cloning, genomic structure, and evalua candidate tumor suppressor gene in myeloid leukemias."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF134157; AAD30106.1; -.

EMBL; AF134157; AAD30106.1; -.

SMART; SM00338; BRLZ; 1.

SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                      MAFE.
Homo sapiens (Human).
- Parvota; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1099 (TrEMBLrel. 16, Last annotation update)
MAFE/KREISLER BASIC REGION/LEUCINE ZIPPER TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                   162 HHHHHHQASPPPSSAASPAQQLPTSHPGPGPHATASATAAGGNGSVEDRFSDDQLVSMSV 221
282
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                       41
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                                                                                                                                                               Local Similarity
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858.5
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1: /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
6: /SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
8: /SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
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18: /SIDSB/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
20: /SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
22: /SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
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24: /SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
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                                                      99.8
99.1
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEIYNKDGNKVDLYGKAVGL.....NKLGVGSDDTVAVGIVYQFA 341
                                                                                                                                                                                                                                                                                                      Length
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                       AAY42550
AAW92998
AAY34058
AAY34057
AAY57356
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AAY37366
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Compugen Ltd.
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Amino acid sequenc
OmpH protein of H.
                            Amino acid
                                         coll wild-type
coll Ompr porin
coll wild-type
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ALIGNMENTS

E. coli wild-type ompF protein. 20-DEC-1999 (first entry) AAY42550;

AAY42550 standard; Protein;

362 ₹

ARESULT ARYST ARYS Bacteria; attenuation; deletion; mutant; vaccine; immune response; Gram negative; infection; diarrhoea; food poisoning; typhoid; salmonellosis; gonorrhoea; gastroenteritis; whooping cough. New attenuated bacteria useful as vaccines for protecting against infections $\,\,$ -WPI; 1999-580447/49. N-PSDB; AAZ22887. Chatfield SN; (PEPT-) PEPTIDE THERAPEUTICS LTD 25-MAR-1998; 25-MAR-1999; 30-SEP-1999. W09949026-A1. Escherichia coli. 98GB-0006449 99WO-GB00935

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RESULT
AAW92998
XX AAW9
AC AAW9
XY 19-y
XX Onpe
KW memk
XX Onpe
KW memk
XX Esc!
XX WO9{
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                  OmpF; porin; amphiphilic alpha-structure; beta-structure; GLUT;
                                                                                                                                                                                                                                       AAW92998 standard; protein; 340
                    WO9618957-A1
                                                     Escherichia coli
                                                                                      membrane
                                                                                                                                      E. coli OmpF
                                                                                                                                                                       19-MAY-1999
                                                                                                                                                                                                      AAW92998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence represents the E. coli wild-type ompF protein. The coding ence of the ompF gene was removed via PCR using primers TT1-TT4
                                                                                                                                                                                                                                                                                                                                       YYFNKNMSTYVDYIINQIDSDNKLGVGSDDTVAVGIVYQF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVDLVNYFEVGAT
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                                                                                                                                                                                                                                                                                                                    yyfnknmstyvdylingidsdnklgvgsddtvavgivyqf 362
                                                                                                                                                                                                                                                                                                                                                                                        tnkftntsgfanktqdvllvaqyqfdfglrpsiaytkskakdvegigdvdlvnyfevgat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \tt dtaysddffvgrvggvatyrnsnffglvdglnfavqylgknerdtarrsngdgvggsisy
                                                                                    protein;
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                                                                                                                                    porin protein.
                                                                                                                                                                     (first entry)
                                                                                      glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.8%; Score 1805; DB 20; Length 362; 100.0%; Pred. No. 9e-148;
                                                                                      transporter

 Mismatches

                                                                                    protein;
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RESULT
AAY42549
ID AAY4
XX AAY4
XX AAY4
XX 20-D
DT 20-D
XX E. C
XX Bact
KW Bact
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method for predicting the tendency of a protein to form either: (a) an amphiphilic alpha-structure or (b) an amphiphilic beta-structure. The methods are used particularly for predicting the structure of membrane proteins such as glucose transporter proteins (GLUTS). They can be used to discern the function of proteins. They can also be used for the rational design or identification of compounds which interact with the proteins or to engineer proteins having particular structures. This sequence represents an Escherichia coli ompf porin which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Predicting tendency to form amphiphilic alpha and beta structures using a novel algorithm to calculate values for subsequent graphical analysis to predict protein structure  \begin{array}{c} \\ \\ \\ \\ \\ \end{array} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-300839/30
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             Bacteria; attenuation; deletion; mutant; vaccine; immune response;
                                         E. coli wild-type ompC protein.
                                                                     20-DEC-1999
                                                                                                                            AAY42549 standard; Protein;
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                                                                                                                                                                                                                                                                     TNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVDLVNYFEVGAT
                                                                                                                                                                                                                                                                                                             eybgfgivgaygaadrtnlqeaqplgngkkaeqwatglkydanniylaanygetrnatpi
                                                                                                                                                                                                                                                                                                                                                                                  DTAYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNERDTARRSNGDGVGGSISY
                                                                                                                                                                                               yyfnknmstyvdylingidsdnklgvgsddtvavglvyqf 340
                                                                                                                                                                                                                                                      \verb|tnkftntsgfanktgdvllvagygfdfglrpsiaytkskakdvegigdvdlvnyfevgat|
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                                                                                                                                                                                                                                                                                                                                                                     dtaysddffvgrvggvatyrnsnffglvdglnfavqylgknerdtarrsngdgvggsisy
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                                                                     (first entry)
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Pred. No. 1.1e-146;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 340;
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Gram negative;

infection; diarrhoea;

food

poisoning; typhoid;

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CC This sequence represents the E. coll wild-type ompC protein. The coding CC sequence of the ompC gene was removed via PCR using primers TT7-TT10 CC (AAX22893-Z22896) to produce a non-reverting deletion mutation. The CC mutant ompC gene (AAX22886) was used in the production of a bacterium CC attenuated by a non-reverting mutation in each of the ompC gene, the arcC gene (AAX22883, AAX22884), and the ompF gene (AAX22887, AAX22888). The CC mutant bacteria provide immunogenic activity with reduced virulence and CC thus can be used as a vaccine for raising an immune response against a CC variety of bacteria in a mammalian host. Such vaccines can provide CC protection against e.g., E. coll (a cause of diarrhoea in humans), CC Salmonella typhimurium (the cause of salmonellassis in several animal CC species), S. typhi (the cause of salmonellosis in several animal CC of food poisoning in humans), S. choleraesuis (a cause of salmonellosis in pigs), S. dublin (a cause of both a systemic and diarrhoeal disease in CC of meningitis), Neisseria gonorrhoeae (a cause of gonorrhoeae), Yersinia CC enterocolitica (the cause of a spectrum of disease in humans ranging CC from gastroenteritis to fatal septicaemic disease in humans ranging CC the cause of whooping cough), and Brucella abortus (a cause of abortion CC bumans) and cause of abortion and infertility in cattle and a condition known as undulant fever in
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Best Local :
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  ylaaqytqtynatrv.
                               YLAANYGETRNATPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDV-E
                                                                                                                                                                 RRSNGDGVGGSISYEYEGFGIVGAYGAADRTNLQE-AQPLGNGKKAEQWATGLKYDANNI
                                                                                                                                                                                                                                                                               DTAYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNERDT-----
                                                                                                                                                                                                                                                                                                                                aevynkdgnkldlygkvdglhyfs----dnkdvdgdqtymrlgfkgetqvtdqltgygq
                                                                                                       lrqngdgvggs1tydyegfg1gga1ssskrtdaqntaay1gngdraetytgg1kydann1
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Pred. No. 9.6e-83;
5; Mismatches 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Braun J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                        WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG 120
                                                                                                                                                                           aevynkdgnkldlygkvdglhyfs----dnkdvdgdqtymrlgfkgetqvtdqltgygq
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Pred. No. 9.6e-83;
5; Mismatches 69;
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bowel disease,
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                                                                                                                       The invention provides a method for diagnosing ulcerative colitis in a subject suspected of having inflammatory bowel disease. The method comprises reacting a patient sample with a porin antigen that is immunologically reactive with paNCA (perinuclear anti-neutrophil cytoplasmic antibodies) and detecting formation of a Ag-pANCA complex as indicative of ulcerative colitis. The method is used to diagnose ulcerative colitis or susceptibility to it. The present sequence represents a E. coll outer membrane protein c precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ulcerative colitis; inflammatory bowel disease; porin antigen; MAb; pANCA; perinuclear anti-neutrophil cytoplasmic antibody; histone H1; outer membrane protein c precursor.
                                                                                                                                                                                                                                                     Diagnosing ulcerative colitis or susceptibility, by detecting complex formation between microbial porin antigen and perinuclear anti-neutrophil cytoplasmic autoantibodies -
                                                                                                                                                                                                                                                                                                                                                                        12-APR-1996;
11-APR-1997;
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                                                        58.1%;
                                             Score 1051; DB 21
Pred. No. 9.6e-83;
5; Mismatches 69
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    The invention provides a method for the diagnosis, prevention and treatment of ulcerative colitis (UC) using histone H1-like antigen, a CC treatment of ulcerative colitis (UC) using histone H1-like antigen. A CC porin antigen or a Bacteroides antigen as a target antigen. The novel comethod of diagnosing UC in a subject suspected of having inflammatory CC protecting the sample with a histone H1-like antigen, or perinuclear CC (2) contacting the sample with a histone H1-like antigen, or perinuclear CC complex of the histone H1-like antigen, or the pawCa-reactive fragment, to form a CC complex of the histone H1-like antigen, or the pawCa-reactive fragment, CC and antibody to the histone H1-like antigen, or the pawCa-reactive fragment, CC indicates that the subject has UC. The pawCa-reactive histone H1-like antigen, porin antigen and Bacteroides antigen are useful in the CC diagnosis, prevention and treatment of UC. The methods can also be used CC for identifying agents useful for treating UC. The present sequence CC represents a E. coli outer membrane protein F precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ulcerative colitis; histone; H1-like antigen; porin antigen; Bacteroides antigen; IBD; pANCA; inflammatory bowel disease; diagnosis; perinuclear anti-neutrophil cytoplasmic antibody; outer membrane protein F precursor.
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                                                                                                                                                                                                                                                                                                   Use of histone H1, porin or Bacteroides antigens as targets for diagnosis, prevention and treatment of ulcerative colitis \,
                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-551215/46.
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Sequence

377

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Similarity

56.9%; Score 1029; DB 20; 56.9%; Pred. No. 7.9e-81; tive 41; Mismatches 79;

Length 377;

38;

Gaps

9;

76 60 Conservative

AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ

weynlqanntessknqsw--trlafaglkfadygsfdygrnygvmydiegwtdmlpefgg

WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG 120

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ARESULT
AAY57355
ID AAY5
XX AAY5
AC AAY5
XX AAY5
XX AAY5
XX AAY5
XX Ulce
KW PANC
KW PANC
XX Use
PD 07-P
PF 12-P
PF 12-P
PF 11-P
XX (REC
XX WPI;
XX WPI;
XX WPI;
XX Diag
PT form
PS Cla:
                              Diagnosing ulcerative colitis or susceptibility, by detecting complex formation between microbial porin antigen and perinuclear anti-neutrophil cytoplasmic autoantibodies -
            Claim 1; Fig 10; 49pp; English
                                                                         WPI; 2000-255695/22
                                                                                                                                       12-APR-1996;
11-APR-1997;
                                                                                                                                                                                           07-MAR-2000
                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                  (REGC ) UNIV CALIFORNIA
                                                                                                                                                                      12-MAR-1998;
                                                                                             Braun J;
                                                                                                                                      96US-0057846
97US-0837058
                                                                                                                                                                      98US-0041889
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Ulcerative colitis; inflammatory bowel disease; porin antigen; MAb; pANCA; perinuclear anti-neutrophil cytoplasmic antibody; histone H1; outer membrane protein F precursor.

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RESULT
AAY34056
ID AAY3
XX AAY3
AC AAY3
XX AAY3
AC AAY3
XX Ulce
KW Ulce
KW Glag
KW Oute
XX Out
XX Out
PI 12-1
XX 12-1
XX 12-1
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Best Local Sim
Matches 209;
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                                                                                                                                                                                                   Ulcerative colitis; histone; H1-like antigen; porin antigen; Bacteroides antigen; IBD; pANCA; inflammatory bowel disease; diagnosis; perinuclear anti-neutrophil cytoplasmic antibody;
 Braun J,
                                                                                                                                                                                      \begin{tabular}{ll} $\text{diagnosis}; perinuclear anti-neutrophil cytoplasmic \\ outer membrane protein F precursor. \end{tabular}
                           (REGC ) UNIV CALIFORNIA
                                                                                                           16-SEP-1999
                                                                                                                                                                                                                                                        E. coli outer membrane protein F precursor.
                                                                                                                                                                                                                                                                                                                                       AAY34056 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                               12-MAR-1999;
                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                  23-NOV-1999
                                                      12-MAR-1998;
                                                                                                                                    W09945955-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             weyniqanntesskngsw--trlafaglkfadygsfdygrnygvmydiegwtdmlpefgg
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 Cohavy O;
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                                                                                                                                                                                                                                                                                  (first entry)
                                                      98US-0041889
                                                                                99WO-US05492
                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.9%; Score 1029; DB 21; 56.9%; Pred. No. 7.9e-81; 7. Mismatches 79;
                                                                                                                                                                                                                                                                                                                                       323
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371

lglvyqf 377

334 VGIVYQF 340

311

ggadnpagvddkdlvkyadigatyyfnknmstyvdykinlideddsfyaangistddiva -----GIGDVDLVNYFEVGATYYENKNMSTYVDYIINQIDSDNKL----GVGSDDTVA 333

370

168 135 121 77 61 22

194

hengdgwglsttydlgmgfsagaaytssdrtndqvnhtaaggdkadawtaglkydanniy

RSNGDGVGGSISYEY-EGFGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIY dsytnadnfmtgrangvatyrntdffglvnglnfavqyqgnnegasngqegtnngrd-vr DT-AYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNE-------RDTAR

LAANYGETRNATPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVE---

latmysetrnmtpfgd---sdyavanktqnfevtaqyqfdfglrpavsflmskgrdlhaa

310

284

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193 167 134

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226

AAY57355;

AAY57355 standard;

Protein;

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13-JUN-2000

(first entry)

coll outer membrane protein F precursor.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a method for the diagnosis, prevention and Ctreatment of ulcerative colitis (UC) using histone H1-like antigen, a porin antigen or a Bacteroides antigen as a target antigen. The novel method of diagnosing UC in a subject suspected of having inflammatory bowel disease (IBD) comprises: (1) obtaining a sample from the subject; (2) contacting the sample with a histone H1-like antigen, or perinuclear anti-neutrophil cytoplasmic antibody (pANCA)-reactive fragment, to form a CC complex of the histone H1-like antigen, or the pANCA-reactive fragment, and antibody to the histone H1-like antigen; and (3) detecting the presence or absence of the complex; where the presence of the complex indicates that the subject has UC. The pANCA-reactive histone H1-like antigen, porin antigen and Bacteroides antigen are useful in the C alagnosis, prevention and treatment of UC. The methods can also be used for identifying agents useful for treating UC. The present sequence crepresents a E. coli outer membrane protein F precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
                                                              Ulcerative colitis; inflammatory bowel disease; porin antigen; MAb; pANCA; perinuclear anti-neutrophil cytoplasmic antibody; histone H1; outer membrane protein F precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                    Escherichia
                                                                                                                             E. coli outer membrane protein F precursor.
                                                                                                                                                              13-JUN-2000 (first entry)
                                                                                                                                                                                              AAY57354;
                                                                                                                                                                                                                            AAY57354 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                           314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 AA;
                                     coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.5%; Score 858.5; DB 20; 57.2%; Pred. No. 3.2e-66; 32. Mismatches 72;
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RESULT
AAW27781
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AC AAW
AC AAW
AC AAW
XX
AC AAW
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AC AM
AC AW

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 174;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a method for diagnosing ulcerative colitis in a subject suspected of having inflammatory bowel disease. The method comprises reacting a patient sample with a porin antigen that is immunologically reactive with pANCA (perinuclear anti-neutrophil cytoplasmic antibodies) and detecting formation of a Ag-pANCA complex as indicative of ulcerative colitis. The method is used to diagnose ulcerative colitis or susceptibility to it. The present sequence represents a E. coli outer membrane protein F precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing ulcerative colitis or susceptibility, by detecting formation between microbial porin antigen and perinuclear anti-neutrophil cytoplasmic autoantibodies
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11-APR-1997;
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                                                                                                                                                                                                                                                    AAW27781 standard; Protein;
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97US-0837058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.5%; Score 858.5; DB 21;
57.2%; pred. No. 3.2e-66;
33. Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                    89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
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7;

Staphylococcus aureus protein; Staphylococcal gene; regulatory

regulatory

ribozyme; y element;

antisense bacterial protein F

sequence; control;
gene expression;

precursor.

Amino acid sequence of an outer membrane

21-JUL-1998 AAW27781;

(first

entry

vaccine;

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RESULT 1
AAYA6025
ID AAY
XX AAY
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XX AAY
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Best Local
                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a Staphylococcus aureus protein, that, based on homology with an Escherichia coli protein, is believed to be a outer membrane protein F precursor. The DNA sequence was isolated from library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Black MT,
Pratt JM,
               Outer membrane protein H; ompH gene; fowl cholera; Pasteurella multocida X-73; porin; avian; vaccine;
 Pasteurella multocida X-73; porin; avian; bacterial porin; H.influenzae porin P2.
                                                     OmpH protein of H.influenza porin P2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 271; 989pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                 29-SEP-1999
                                                                                                              AAY26025;
                                                                                                                                      AAY26025 standard;
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 to isolate antimicrobial compounds, and in vaccines against S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-FEB-1997;
                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                     1997-424969/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ne; Staphylococcal infection; food poisoning; scaled skin syndrome; shock syndrome.
                                                                                                                                                                                                                                                              Similarity
52; Conser
                                                                                                                                                                                                                                                                                                                                89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burnham MK,
Reichard RW,
                                                                                                                                                                                                                                                              Conservative
                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-
                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                         15.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "residues designated X are not defined the specification"
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                                                                                                                                       353
                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                           Score 276; DB 18;
Pred. No. 9.6e-17;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                      Length
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              molecular sieve;
veterinary medic
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RESULT 1

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AAY26023 standard; Protein;

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Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane protein that is involved in pore formation. They serve as molecular sieves that allow polar solutes to pass through, but excludes non-polar molecules of comparable sizes. This amino acid sequence shares a sequence homology of about 38% to Pasteurella multocida X-73 OmpH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glisson JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1998;
08-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein. Peptides derived from the P.multocida OmpH protein are useful in the production of protective vaccines for use in vertebrates in particular, for prevention of fowl cholera and for diagnosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present amino acid sequence is that of the Haemophilus influenzae porin P2. This protein is a bacterial porin which is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 5; 119pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  veterinary medicine.
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                                                                                                                                                   220
                                                                                                                                                                                  177
303 havlfgi 309
                          330 DTVAVGI 336
                                                        251 gyaktknk----adkhekryfvspgfqyelmedtnlygnlkyerinsvdqgekv---re
                                                                                       274 AYTKSKAKDVEGIGDVDLVNYF-EVGATYYFNKNMSTY--VDY-IINQIDSDNKLGVGSD
                                                                                                                                                                                                                                                                        100 RNYGVVYDALGYTDMLPEFGGDTAYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLG
                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                            1 AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTY--ARLGFKGETQINSDLTGY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding Pasteurella multocida outer membrane protein {\tt H}, useful delivering peptide epitopes for vaccines against fowl cholera
                                                                                                                                                 YDANNIYLAANYGETRNATPITNKFTNTSGFANKTQDV---LLVAQYQF-DFGLRPSI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1999-385575/32
                                                                                                                   ydannivagfaygr----
                                                                                                                                                                                                            KNERDTARRSNGDGVGGSISYEYEGFGIVGAYGAADRINLQEAQPLGNGKKAEQWATGLK
                                                                                                                                                                                                                                         keygviek----nsyiptegnaiay-----tykg-----iegltlgasyv-
                                                                                                                                                                                                                                                                                                   gyyetrfinkdidgneknigsgfgsittklayaglgnkelgeatfglqktiadkistaed
                                                                                                                                                                                                                                                                                                                                  GQWEYNFQGNNSEGADAQTGN----KTRLAFAGLKYADVGSFDYG----
                                                                                                                                                                                                                                                                                                                                                              avvynnegtkvelggrvsiiaeqstsnrkdqkhqhgslrnqgsrfnikvthnlgdgyyal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Luo Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0120051
97US-0067957
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                                                                                                                                                                                                                                                                                                                                                                                                                                           23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 170.5;
Pred. No. 7.7
                                                                                                                   tnykaqqaktqqvngalatlgyhfddlgllislds
                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            .7e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                           109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         353;
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                           302
                                                                                         329
                                                                                                                                                                                  201
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                                                                                                                                                                                                                                            176
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                                                                                                                      250
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14;

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cc multocida x-73, outer membrane protein H (OmpH). This protein is a cc porin, which is a major outer membrane protein that is involved in correct formation. They serve as molecular sieves that allow polar solutes ct pass through, but excludes non-polar molecules of comparable sizes. The amino acid composition is typical of non-specific bacterial porins cwith highly negative hydropathy index, high glycine content, low proline content and lack of cysteine. This amino acid sequence shows homology of about 38% to bacterial porins, like that of H.influenzae porin P2. Cc Multiple antigen peptides are synthesised from the loop 2 and loop 5 cregions of the protein that can be used for immunisation of the fowls to induce heterologous protection against P.multocida infection. This sequence can be used for diagnostic assays for use in veterinary medicine, especially for the diagnosis of fowl cholera, caused by P.multocida. Peptides derived from the ompH protein are useful in the protective vaccines for use in vertebrates, in particular for the four contents of the course o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Fig 4; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glisson JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1998;
08-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OmpH protein of Pasteurella multocida X-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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prevention of fowl cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present amino acid sequence is that of the avian Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding Pasteurella multocida outer membrane protein delivering peptide epitopes for vaccines against fowl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999-385575/32
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97US-0067957.
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81..11
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18..20
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12..14
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217..238
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/note- "Hydrophobic amino acids"
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RESULT 1
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19-DEC-1988;
06-JAN-1989;
06-JAN-1989;
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                                           Meningococcus class 1 outer-membrane protein vaccine -
                                                                                                                                      SEID RC, PARADISO PR, VANDERLEY P, HECKELS
                                                                                                                                                                                                                      (VOLK-)
                                                                                                                                                                                                                                             (PRAX-)
                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-1989;
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                                                                                            PI; 1990-224326/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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88NL-0003111.
89NL-0000030.
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22.9%;
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                                                                                                                                                                     POOLMAN JT,
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; Pred. No. 3.8e-06;
39; Mismatches 150;
                                                                                                                                             CLARKE IN;
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                                                                                                                                                                     HOOGERHOUT
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immunise against meningococcal disease

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Best Local S
Matches 79
                                                                                                                                                                   Blake MS,
Tai JY;
                             High expression of outer membrane meningococcal group B porin proteins - and fusion proteins in Escherichia coli, and purification method; for use in vaccines against Neisseria meningitidis and in research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptides derived from outer membrane, encoding homo/heterologous product such as a antigen-flagelin fusion protein, are useful in eliciting a strong and wide ranging immune response against most
                                                                                                                WPI; 1995-075239/10.
N-PSDB; AAQ85391.
                                                                                                                                                                                                                                                                    23-JUL-1993;
                                                                                                                                                                                                                                                                                                                                      02-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR70763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR70763 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                (NAVA-) NORTH AMERICAN VACCINE (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                     22-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; ; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274
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les 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVDLVNYFE----VGATYYFNKNMSTYV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ataayrfg-nvtprvsyahgfkakvngvkd---anyqqdqv1vgadydfskrtsalv 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nahpv··-kdyqvhrvvagydandlyvsvagqyeaakn----nevgstkgkkhqtq-va 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yvprdnandvdkykhtkssresyhaglkyenagffgqyagsfakyadlntdaervavnta 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agnlntvlkdsgdnvnawesgsnt--edvlglgtigrvesreisvrydspvfagfsgsvq 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --NYGVVYDALGYTDMLPEFGGDTAYSDDFFVGRVGGVATYRNSNFFG--LVDGLNFAVQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          skigfkgqedlgnglkaiwqle---qkasiagtnsgwgn--rqsfiglk----ggfgtvr 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARLGFKGETQINSDLTGYGQWEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAOPLGNGKKAEOWATGLKYDANNIY - - LAANYGETRNATPITNKFTNTSGFANKTODVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLGK---NERDTARRSNGDGVGGSISYEYEGFGIVGAYGA-----ADR--TNLQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                     porin protein; meningococcal; outer membrane protein;
; meningitis; Neisseria menigitidis; PCR primer.
                                                                                                                                                                                  Hronowski LJJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                    9305-0096182
                                                                                                                                                                                                                                                                                                     94WO-US08327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.0%; Score 162; DB 11;
26.6%; Pred. No. 4.2e-06;
htive 42; Mismatches 126;
                                                                                                                                                                                  Liang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342
                                                                                                                                                                                                                                   INC
                                                                                                                                                                                  Pullen JK,
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                                                                                                                                                                                  HL;
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Example; Figure 9; 81pp; English

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RESULT 15
AAW21742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The example concerns cloning of Class 2 porin from Group B

(Nelsseria meningitidis strain BNCW M986 serotype 2a (see

AAQ85300, AAQ85301). The plasmid pET-17b was used to express the

Class 2 porin. A plasmid was designed to yield a mature class 2

porin. The mature class 2 porin was constructed by amplifying

the pUC19 class 2 porin construct using the oligos AAQ85302 and

CAAQ85303. This strategy allowed the cloning of the amplified class 2

porin into the NdeI and XhoI sites of the plasmid pET-17b thus

producing mature class 2 porin. Std. PCR was conducted using the

UC19 class as the template and the two oligos. The PCR reaction

yielded a 1.1kb product. The DNA obtd. was purified and digested

with NdeI and XhoI and ligated to pET-17b, and used to transform

E.coli. DNA from transformed clones was sequenced. AAQ85391,R70763

show the nt and translated AA sequence of the mature class II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                13-JUN-1996;
01-FEB-1996;
                                                                   31-JAN-1997;
                                                                                                    07-AUG-1997
                                                                                                                                                                                                        Porin protein;
meningitis; va
                                                                                                                                                                                                                                                                                                09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                   AAW21742 standard; Protein; 342
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                                                                                                                                        W09728273-A1
                                                                                                                                                                      Neisseria meningitidis
                                                                                                                                                                                                                                                           Neisseria meningitidis class 3 mature porin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         porin gene cloned into the expression plasmid pET-17b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 kakvngvkd---anygydqvivgadydfskrtsalv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 andlyvsvaggyeaakn----nevgstkgkkheqtqvaataayrfg-nvtprvsyahgf 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 ANNIY--LAANYGETRNATPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 syhaglkyenagffgqyagsfakyadlntdaervavntanahpv---kdyqvhrvvagyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 GGSISYEYEGFGIVGAYGA------ADR--TNLQEAQPLGNGKKAEQWATGLKYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 GDTAYSDDFFVGRVGGVATYRNSNFFG--LVDGLNFAVQYLGK---NERDTARRSNGDGV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 AKDVEGIGDVDLVNY----FEVGATYYFNKNMSTYV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 EYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGR--NYGVVYDALGYTDMLPEFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 VDLYGKAVGLHYFSKGNGENSYGGNGDMTY----ARLGFKGETQINSDLTGYGQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 vtlygtikagvevsrvkdagtykaqggksktatqiadfgskigfkgqedlgngmkaiwql
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e---gkaslagtnsgwgn--rqsfiglk----ggfgtvragnlntvlkdsgdnvnawesg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 AA;
                                                                                                                                                                                                        in; porB gene; outer membrane
vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                              (first entry)
                96US-0020440.
96US-0010972.
                                                                 97WO-US01687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.7%;
24.7%;
                                                                                                                                                                       serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 157; DB 16;
; Pred. No. 1.1e-05;
45; Mismatches 150;
                                                                                                                                                                                                                           protein;
                                                                                                                                                                         8765 (B:15:P1,3)
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(NAVA-) NORTH AMERICAN VACCINE INC.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This protein comprises the mature class 3 porin (MB3) protein porB CC from group B Neisseria meningitidis, encoded by a mature class 3 CC porin gene (see AAT77815) in vector pET-24a and expressed in E. coli DH5-alpha transformants. A method is claimed for the high level capression of an outer membrane meningococcal group B porin protein CC in yeast. It comprises: ligating a DNA sequence encoding mature porin (see AAT77812), or mature porin fused to a scoretion signal CC sequence (see AAT77814), into a vector containing a selectable marker and a yeast promoter such as the AOX1 promoter; using the vector to CC and a yeast promoter such as the AOX1 promoter; using the vector to claimed for purifying the perin pastoris, host cells; and CC claimed for purifying the porin protein. The level of porin CC claimed for purifying the porin protein. The level of porin protein senhanced by optimising the 5' region of the porin protein expression is enhanced by optimising the 5' region of the porin protein gene for yeast codon usage (see AAT76738 and AAT77816).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.7%; Score 157; DB 18; Length 342; Best Local Similarity 24.7%; Pred. No. 1.1e-05; Matches 83; Conservative 45; Mismatches 150; Indels 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    production of meningococcal group B porin proteins in yeast - by
extraction of a porin protein, or porin protein fused to a yeast
secretion signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-402625/37.
N-PSDB; AAT77815-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N. meningitidis (claimed).
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Tai JY, Wang M, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                               172 syhaglkyenagffgqyagsfakyadlntdaervavntanahpv---kdyqvhrvvagyd 228
                                                                                                                                                                                                                                                114 snt--edvlglgtigrvesreisvrydspvfagfsgsvqyvprdnandvdkykhtkssre 171
                                                                                                                                                                                                                                                                          283
                                       280 AKDVEGIGDVDLVNY----FEVGATYYFNKNMSTYV 311
                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 VDLYGKAVGLHYFSKGNGENSYGGNGDMTY-----ARLGFKGETQINSDLTGYGQW 61
                                                                                                                                                                                                                                                                                                                                                                                                                     ω
                                                                              andlyvsvaggyeaakn----nevgstkgkkheqtqvaataayrfg-nvtprvsyahgf 282
                                                                                                                        ANNIY--LAANYGETRNATPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSK 279
                                                                                                                                                                                                      GGSISYEYEGFGIVGAYGA-----ADR--TNLQEAQPLGNGKKAEQWATGLKYD 221
                                                                                                                                                                                                                                                                                                                                                                                                                   vtlygtikagvevsrvkdagtykagggksktatgiadfgskigfkggedlgngmkaiwql 62
kakvngvkd---anyqydqvivgadydfskrtsalv
                                                                                                                                                                                                                                                                                                                                  e---qkasiagtnsgwgn--rqsfiglk----ggfgtvragnlntvlkdsgdnvnawesg
                                                                                                                                                                                                                                                                                                                                                        EYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGR--NYGVVYDALGYTDMLPEFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 AA;
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                                                                                                                                                                                                                                                                                                                                         113
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Search completed: July Job time: 444 sec

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Perfect score:
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Gapop 10.0 ,
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141.869 Million cell updates/sec
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1809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
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US-09-041-889-28
US-08-096-182A-4
US-08-98-760-4
PCT-US94-08327-4
US-08-877-109-6
US-08-98-78-760-6
PCT-US94-08327-2
US-08-98-182A-2
US-08-98-181A-12
US-08-98-181A-14
PCT-US94-08326-14
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Compugen Ltd.
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                                            28. Appli
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ALIGNMENTS

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; OTHER INFORMATION: US-08-355-844-1
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GENERAL INFORMATION:
                                                                                                                                                                                             TELEPHONE: 212-408-2586
TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
                                                                                                                                                                                                                                                                    CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Tang, Henry Y.S.
REGISTRATION NUMBER: 29,705
REFERENCE/DOCKET NUMBER: A299
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-586
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOSITION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cheung, TITLE OF INVENTION:
                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                 NAME/KEY:
LOCATION:
                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 14-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond STREET: 30 Rockefeller Plaza
                                                                                       ORGANISM:
                                                                                                                                                                              TYPE: amino acid
                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08355844
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Iserovich, Pavel
                                     Peptide
1..340
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                                                                                                                                          linear
                                                                                       Escherichia
                                                                                                                     peptide
                                                                                                                                                             single
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                  OmpF porin protein
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                           TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO:
                                                                    REGISTRATION NUMBER: 29,705
REFERENCE/DOCKET NUMBER: A29927-50/29910
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2586
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRECORPATIBLE
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fischbarg, Jorge
APPLICANT: Czegledy, Ferenc
APPLICANT: Iserovich, Pavel
                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Tang, Henry Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue &
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cheung, Min
TITLE OF INVENTION: A METHOD :
TITLE OF INVENTION: STRUCTURE
            SEQUENCE CHARACTERISTICS: LENGTH: 340 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10112-0228
                                                                                                                                                                                                                                                                                                                                                                                 STATE: NEW YORK
                                                                                                                    NAME: Tang, Henry Y.S. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ
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acid
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99.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A METHOD FOR PREDICTING PROTEIN
                                                                                                                                                                                   US 08/355,844
                                                                                                                                                                                                                                              PCT/US95/16126
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Pred. No. 26
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US-09-041-889-30
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Best Local Sim
Matches 338;
                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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ORIGINAL SOURCE:
ORGANISM: ESC
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                          APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subty;
TITLE OF INVENTION: Microbial UC pANCA antigens
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                       ZIP:
                                                                                                                                                                                                             CITY: San Diego
STATE: California
                                                                   CLASSIFICATION:
                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYBGFGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAANYGETRNATPI
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                                                                                                                                                                                                                                                                                                                                                                        6033864
                                                                                                                                                                                                                                       E: Campbell & Flores LLP
4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                     Application US/09041889
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linear
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99.4%;
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                                         US 08/837,058
                                                                                            US/09/041,889
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Pred. No. 2e-159;
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                                                                                                                                                                                                                                          Suite 700
                                                                                                                         #1.25
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US-09-041-889-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.1%;
Best Local Similarity 58.9%;
Matches 212; Conservative 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subty
TITLE OF INVENTION: Microbial UC panca antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                     CITY: San Diego
STATE: California
                                                                                                                                                                                                                         ZIP: 92122
                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                        STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRONGDGVGGSITYDYEGFGIGGAISSSKRTDAONTAAYIGNGDRAETYTGGLKYDANNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRSNGDGVGGSISYEYEGFGIVGAYGAADRTNLQE-AQPLGNGKKAEQWATGLKYDANNI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTYGSDNFMQQRGNGFATYRNTDFFGLVDGLNFAVQYQGKNGNPSGEGFTSGVTNNGRDA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEVYNKDGNKLDLYGKVDGLHYFS-----DNKDVDGDQTYMRLGFKGETQVTDQLTGYGQ 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLAAQYTQTYNATRV-----GSLGWANKAQNFEAVAQYQFDFGLRPSLAYLQSKGKNLGR 308
                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                            Campbell & Flores LLP
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Pred. No. 2.9e-90;
5; Mismatches 69
                                                                                                                                 Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 28, Patent No. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 535-89
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                       APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosi
TITLE OF INVENTION: Ulcerati
TITLE OF INVENTION: MICROBIA
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 VGIVYQF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 GGADNPAGVDDKDLVKYADIGATYYFNKNMSTYVDYKINLIDEDDSFYAANGISTDDIVA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 HENGDGWGLSTTYDLGMGFSAGAAYTSSDRTNDQVNHTAAGGDKADAWTAGLKYDANNIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 LGLVYQF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 LATMYSETRNMTPFGD---SDYAVANKTQNFEVTAQYQFDFGLRPAVSFLMSKGRDLHAA 310
                                                                                                                                               STREET: 4370 La
CITY: San Diego
STATE: Californ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                             COUNTRY: USA
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AEIYNKDGNKYDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DT-AYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNE------RDTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GIGDVDLVNYFEVGATYYFNKNMSTYVDYIINQIDSDNKL----GVGSDDTVA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSYTNADNFMTGRANGVATYRNTDFFGLVNGLNFAVQYQGNNEGASNGQEGTNNGRD-VR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEVYNKDGNKLDLYGKVDGLHYFSDNSAK-----DGDQSYARLGFKGETQINDQLTGYQQ
                                                                                                                                                                                                                                                                                                                                                                                8, Application US/09041889
6033864
                                                                                                                                                   California
                                                                                                                                                                                    4370 La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (619) 535-8949
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                                                                                                                                                                                      Campbell & Flores LLP
70 La Jolla Village Drive,
                                                                                                                                                                                                                                                              Microbial UC panCa
                                                                                                                                                                                                                                                                                Diagnosis, Prevention and Treatment of Ulcerative Colitis, and Clinical Subtypes Thereof, Using
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                   Version
                                                                                                                                                                                      Suite 700
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                   #1.25
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; MOLECULE TYPE: peptide US-09-041-889-28
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Best Local Similarity
Matches 174; Conserv
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APPLICATION NUMBER: US 08/837

FILING DATE: 11-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: 9-PM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08096182A Patent No. 5439808
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
                                                                                                           APPLICANT: Hronowski Lucjan J.J.
APPLICANT: Pullen, Jeffrey K.
TITLE OF INVENTION: Method for the
TITLE OF INVENTION: Purification an
TITLE OF INVENTION: Porin Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                               APPLICANT: Blake, Milan S
APPLICANT: Tai, Joseph Y.
APPLICANT: Qi, Huilin L.
                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 HENGDGWGLSTTYDLGMGFSAGAAYTSSDRTNDQVNHTAAGGDKADAWTAGLKYDANNIY
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                           STREET: 1100 New CITY: Washington STATE: D.C.
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COUNTRY: U
ZIP: 20005
                                                                       ADDRESSEE: Sterne, Kessler, Goldstein & STREET: 1100 New York Ave., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSNGDGVGGSISYEY-EGFGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIY 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAANYGETRNATPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGI 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DT-AYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNE------RDTAR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDVD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEYNIQANNTESSKNQSW--TRLAFAGLKFADYGSFDYGRNYGVMYDIEGWTDMLPEFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                               Liang, Shu-Mei
                                                                                                                                                                                                                                                                                                       Blake, Milan S.
                 USA
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                                                                                                                                                Method for the High Level Expression,
Purification and Refolding of the Outer Membrane Group B
Porin Proteins from Neisseria Meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/837,058
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R: P-PM 3006
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57472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
                      APPLICANT: Tai, Joseph ..

APPLICANT: Qi, Hullin L.

APPLICANT: Liang, Shu-Mei

APPLICANT: Liang, Shu-Mei

APPLICANT: Liang, Shu-Mei

APPLICANT: Honowski, Lucjan J.J.

APPLICANT: Pullen, Jeffrey K.

TITLE OF INVENTION: Method for the High Level Expression,

TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B

TITLE OF INVENTION: Porin Proteins from Neisseria meningitidis

TITLE OF INVENTION: Porin Proteins from Neisseria meningitidis
                                                                                                                                                                                                                                                                                                           APPLICANT: Blake, Milan S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08 FILING DATE: 23-UUL-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 ANNIY--LAANYGETRNATPITNKETNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 SYHAGLKYENAGFFGQYAGSFAKYADLNTDAERVAVNTANAHPV---KDYQVHRVVAGYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 SNT--EDVLGLGTIGRVESREISVRYDSPVFAGFSGSVQYVPRDNANDVDKYKHTKSSRE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 AKDVEGIGDVDLVNY----FEVGATYYFNKNMSTYV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 KAKVNGVKD---ANYQYDQVIVGADYDFSKRTSALV 315
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VTLYGTIKAGVEVSRVKDAGTYKAQGGKSKTATQIADFGSKIGFKGQEDLGNGMKAIWQL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGSISYEYEGFGIVGAYGA-----ADR--TNLQEAQPLGNGKKAEQWATGLKYD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDTAYSDDFFVGRVGGVATYRNSNFFG--LVDGLNFAVQYLGK---NERDTARRSNGDGV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E---QKASIAGTNSGWGN--RQSFIGLK----GGFGTVRAGNLNTVLKDSGDNVNAWESG
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Washington
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                                                                                                                                                           US-08-798-760-4
                                                                                                                    Sequence 4, Application US/08798760 Patent No. 6013267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                               GENERAL INFORMAPPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/877,109
                                        APPLICANT:
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FILING DATE: 28-APR-1995
APPLICATION NUMBER: 08/096,182
FILING DATE: 23-JUL-1993
ANTONNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                      229
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                                                                                                                                                                                                                                                                                                                                                                                                                                     175 GGSISYEYEGFGIVGAYGA------ADR--TNLQEAQPLGNGKKAEQWATGLKYD 221
                                                                                                                                                                                                                                         283 KAKVNGVKD---ANYQYDQVIVGADYDFSKRTSALV
                                                                                                                                                                                                                                                                             280 AKDVEGIGDVDLVNY----FEVGATYYFNKNMSTYV 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: ESMOND, ROBERT W. REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 20005
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                                  L INFORMATION:
JICANT: Blake, Milan S.
JICANT: Tal, Joseph Y.
JICANT: Q1, Huilin L.
                                                                                                                                                                                                                                                                                                                    ANDLYVSVAGQYEAAKN-----NEVGSTKGKKHEQTQVAATAAYRFG-NVTPRVSYAHGF 282
                                                                                                                                                                                                                                                                                                                                                       ANNIY -- LAANYGETRNATPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSK 279
                                                                                                                                                                                                                                                                                                                                                                                                  SYHAGLKYENAGFFGQYAGSFAKYADLNTDAERVAVNTANAHPV---KDYQVHRVVAGYD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNT--EDVLGLGTIGRVESREISVRYDSPVFAGFSGSVQYVPRDNANDVDKYKHTKSSRE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDTAYSDDFFVGRVGGVATYRNSNFFG--LVDGLNFAVQYLGK---NERDTARRSNGDGV 174
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Liang, Shu-Mei
Hronowski, Lucjan J.J.
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LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-798-760-4
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RESULT 9
PCT-US94-08327-4
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 11-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                222 ANNIY--LAANYGETRNATPITNKFTNTSGFANKTQDVLLVAQYQFDEGLRPSIAYTKSK 279
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                                                                                              283 KAKVNGVKD---ANYQYDQVIVGADYDFSKRTSALV 315
                                                                                                                                         280 AKDVEGIGDVDLVNY----FEVGATYYFNKNMSTYV 311
                                                                                                                                                                                  229 ANDLYVSVAGQYEAAKN-----NEVGSTKGKKHEQTQVAATAAYRFG-NVTPRVSYAHGF 282
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REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 14
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COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 E---QKASIAGTNSGWGN--RQSFIGLK----GGFGTVRAGNLNTVLKDSGDNVNAWESG 113
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1100 New York Ave., Suite 600
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Purification and Refolding of the Outer Membrane Group
Porin Proteins from Neisseria Meningitidis
23
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Sequence 4, Application PC/TUS9408327 GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

The Rockefeller University 1230 York Avenue New York, New York 10021

APPLICANT:

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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                              172 SYHAGLKYENAGFFGQYAGSFAKYADLNTDAERVAVNTANAHPV----KDYQVHRVVAGYD
229 ANDLYVSVAGQYEAAKN----NEVGSTKGKKHEQTQVAATAAYRFG-NVTPRVSYAHGF 282
                                     222 ANNIY--LAANYGETRNATPITNKETNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSK 279
                                                                                                                                                            114 SNT--EDVLGLGTIGRVESREISVRYDSPVFAGFSGSVQYVPRDNANDVDKYKHTKSSRE 171
                                                                                                                                                                                               120 GDTAYSDDFFVGRVGGVATYRNSNFFG--LVDGLNFAVQYLGK---NERDTARRSNGDGV 174
                                                                                                                                                                                                                                          63 E---QKASIAGTNSGWGN--RQSFIGLK----GGFGTVRAGNLNTVLKDSGDNVNAWESG 113
                                                                                                                                                                                                                                                                                  62 EYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGR--NYGVVYDALGYTDMLPEFG
                                                                                                                                                                                                                                                                                                                                                                11 VDLYGKAVGLHYFSKGNGENSYGGNGDMTY-----ARLGFKGETQINSDLTGYGQW 61
                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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ZIP: 20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                   GGSISYEYEGFGIVGAYGA------ADR--TNLQEAQPLGNGKKAEQWATGLKYD 221
                                                                                                                                                                                                                                                                                                                          VTLYGTIKAGVEVSRVKDAGTYKAQGGKSKTATQIADFGSKIGFKGQEDLGNGMKAIWQL 62
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                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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1100 New York Ave.,
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/ENTION: Method for the High Level
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United States of America
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Hronowski, Lucjan J.J.
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Porin Proteins from Neisseria Meningitidis
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Suite 600
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SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acid
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APPLICANT: Pullen, Jeffrey K.

TITLE OF INVENTION: Method for the High Level Expression, TITLE OF INVENTION: Purification and Refolding of the Out TITLE OF INVENTION: Porin Proteins from Neisseria Meninging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE, DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
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APPLICANT:
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,
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CTTY: Washington
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                                                                                                           135 SNT--EDVLGLGTIGRVESREISVRYDSPVFAGFSGSVQYVPRDNANDVDKYKHTKSSRE 192
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                                    193 SYHAGLKYENAGFFGQYAGSFAKYADLNTDAERVAVNTANAHPV---KDYQVHRVVAGYD
                                                                        175
222 ANNIY--LAANYGETRNATPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSK 279
                                                                                                                                             120 GDTAYSDDFFVGRVGGVATYRNSNFFG--LVDGLNFAVQYLGK---NERDTARRSNGDGV 174
                                                                                                                                                                                                         62 EYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGR--NYGVYYDALGYTDMLPEFG 119
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                          24 VTLYGTIKAGVEVSRVKDAGTYKAQGGKSKTATQIADFGSKIGFKGQEDLGNGMKAIWQL 83
                                                                                                                                                                                                                                                                                             11 VDLYGKAVGLHYFSKGNGENSYGGNGDMTY-----ARLGFKGETQINSDLTGYGQW 61
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Qi, Huilin L.
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Porin Proteins from Neisseria Meningitidis
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Pred. No. 6.7e-07;
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US-08-877-109-6
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                                                                                                                                                                                              Matches
                                                                                                                                                                                                                   Query Match
Best Local :
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TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
TEC. 1827 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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MEDIUM TYPE: Floppy disk
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APPLICANT: Pullen, Jeffrey K.
TITLE OF INVENTION: Method for th
TITLE OF INVENTION: Purification;
TITLE OF INVENTION: Porin Protein
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PRIOR APPLICATION DATA:
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120 GDTAYSDDFFVGRVGGVATYRNSNFFG--LVDGLNFAVQYLGK---NERDTARRSNGDGV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TILING DATE: 23-JUL-1993
TTORNEY/AGENT INFORMATION:
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FILING DATE: 28-APR-1995
APPLICATION NUMBER: 08/0
                                                                                                                                                       11 VDLYGKAVGLHYFSKGNGENSYGGNGDMTY-----ARLGFKGETQINSDLTGYGQW 61
                                                                                                                                                                                            Local Similarity 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/877,109 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
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                                    E---QKASIAGTNSGWGN--RQSFIGLK----GGFGTVRAGNLNTVLKDSGDNVNAWESG
                                                                                                                VTLYGTIKAGVEVSRVKDAGTYKAQGGKSKTATQIADFGSKIGFKGQEDLGNGMKAIWQL 83
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                                                                         EYNFOGNNSEGADAOTGNKTRLAFAGLKYADVGSFDYGR--NYGVVYDALGYTDMLPEFG
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5. 5747287
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1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                       363 amino acids
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                                                                                                                                                                                            8.7%; Score 157; DB 1; Length 363; 24.7%; Pred. No. 6.7e-07; tive 45; Mismatches 150; Indels
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ork Ave., NW
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Patent No.
                                                                                                                                      Matches
                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ITITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
62 EYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGR--NYGVVYDALGYTDMLPEFG
                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 11-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
                                                          24 VTLYGTIKAGVEVSRVKDAGTYKAQGGKSKTATQIADFGSKIGFKGQEDLGNGMKAIWQL 83
                                                                                          11 VDLYGKAVGLHYFSKGNGENSYGGNGDMTY-----ARLGFKGETQINSDLTGYGQW 61
                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
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VERWION: Method for the High Level Expression,
VERNION: Method for the High Level Expression,
VERVION: Purification and Refolding of the Outer Membrane Group
VERVION: Porin Proteins from Neisseria Meningitidis
EQUENCES: 23
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Qi, Huilin L.
                                                                                                                                      Conservative
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                                                                                                                                                        24.78;
                                                                                                                                                    8.7%; Score 157; DB 3; 24.7%; Pred. No. 6.7e-07;
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RESULT 13
PCT-US94-08327-6
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                                                                                                               TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/096.

FILING DATE: 23 July 1993

ATTORNEY_AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08327
FILING DATE: Herewith
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
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TITLE OF INVENTION:
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                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 1438.006PC00 TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein
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                         TOPOLOGY:
                                            TYPE: amino acid
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                                                                                                                                                           TELEPHONE:
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Beltsville, Maryland 20705
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Method for the High Level
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US-08-096-182A-2
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Best Local
TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                            REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pullen, Jeffrey K.
TITLE OF INVENTION: Method for the High Level Expression,
TITLE OF INVENTION: Purification and Refolding of the Out
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                                                          TELEPHONE:
                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 23-JUI
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83; Conserv
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1100 New York Ave.,
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Qi, Huilin L.
Liang, Shu-Mei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blake, Milan S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hronowski, Lucjan
                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                            (202) 371-2600
                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                     NFORT W. Robert W. 32,893
                                                                                                                                                                                              23-JUL-1993
                                         371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.78;
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                                                                                                                                                                                                                 US/08/096,182A
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                                                                                                   1438.0060000
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Pred. No. 6.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J.J.
                                                                                                                                                                                                                                                                                                                                                                                                                             Goldstein & Fox Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Outer Membrane Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
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; MOLECULE TYPE: protein US-08-096-182A-2

TYPE: amino acid TOPOLOGY: linear

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US-08-877-109-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.2%; Score 147.5; DB 1; Length 309; Best Local Similarity 25.1%; Pred. No. 4.1e-06; Matches 76; Conservative 46; Mismatches 116; Indels 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Blake, Milan S.
APPLICANT: Tai, Joseph Y.
                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/877,109
                     PRIOR APPLICATION NUMBER: 08/431,264
APPLICATION NUMBER: 08/431,264
FILING DATE: 28-APR-1995
APPLICATION NUMBER: 08/096,182
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Llang, Shu-Mei
APPLICANT: Hronowski, Lucjan J.J.
APPLICANT: Pullen, Jeffrey K.
TITLE OF INVENTION: Method for th
TITLE OF INVENTION: Purlfication.
TITLE OF INVENTION: Porin Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 TYV 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 ADRTNLQEAQPLGNGK-KAEQWATGLKYDANNIYLAANYGETRNATPITNKFTNTSGFAN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 LISVRYDSPEFAGLSGSVQYAL-----NDNAGRHNSESYHAGFNYKNGGFFV--QYGG 172
                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 NGDMTY------ARLGFKGETQINSDLTGYGQWEYNFQGNNSEGADAQTGNKTRL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEG-IGDVDLVNYFE---VGATYYFNKNMS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYKRHHQVQEGLNIEKYQIHRLVSG--YDNDALY-ASVAVQQQDA-----KLTDASNSHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --VATYRNSNFFGLVDGLNFAVQYLGKNERDTARRSNGDGVGGSISYEYEGFGIVGAYGA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFIGLK-GGFGKLRVGRLNSVLKDT------GDINPWDSKSDYLGVNKIAEPEAR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGOVTEVTTATGIVDLGSKIGFKGQEDLGNGLKAIWQVE---QKASIAGTDSGWGN--RQ 73
Esmond,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Sterne, Kessler,
1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                      USA
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Q1, Huilin L.
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Purification and Refolding of the Outer Membrane Group B
Porin Proteins from Neisserla meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Mismatches 116; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goldstein & Fox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0060001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
                                     225
                                                                                                                 173 AYKRHHQVQEGLNIEKYQIHRLVSG--YDNDALY-ASVAVQQQDA-----KLTDASNSHN
309 TYV 311
                                                                           253 KTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEG-IGDVDLVNYFE----VGATYYFNKNMS
                                                                                                                                                       194 ADRTNLQEAQPLGNGK-KAEQWATGLKYDANNIYLAANYGETRNATPITNKFTNTSGFAN 252
                                                                                                                                                                                                 122 LISVRYDSPEFAGLSGSVQYAL-----NDNAGRHNSESYHAGFNYKNGGFFV--QYGG 172
                                                                                                                                                                                                                                                                                                                                                               19 NGQVTEVTTATGIVDLGSKIGFKGQEDLGNGLKAIWQVE---QKASIAGTDSGWGN--RQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                               74 SFIGLK-GGFGKLRVGRLNSVLKDT------GDINPWDSKSDYLGVNKIAEPEAR 121
                                                                                                                                                                                                                                                                                                                     84 AFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGGD----TAYSDDFFVGRVGG---- 135
                                                                                                                                                                                                                                                                                                                                                                                                   35 NGDMTY------ARLGFKGETQINSDLTGYGQWEYNFQGNNSEGADAQTGNKTRL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 76; Conserv
                                     SQTEVAATLAYRFG-NVTPRVSY----AHGFKGLVDDADIGNEYDQVVVGAEYDFSKRTS
                                                                                                                                                                                                                                       --VATYRNSNFFGLVDGLNFAVQYLGKNERDTARRSNGDGVGGSISYEYEGFGIVGAYGA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 147.5; DB 1;
Pred. No. 4.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 309;
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Search completed: July 3, 2001, 14:56:46
Job time: 536 sec

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
Query
Match
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Gapop 10.0 , Gapext 0.5
     US-09-490-291-9
1809
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ALIGNMENTS

A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-362 <blats 21="" a;cross-references:="" a;experimental="" a;gene:="" a;map="" c;complex:="" c;genetics:="" cmlb;="" coa;="" cry="" gb:ae000195;="" gb:u00096;="" homotrimer<="" k-12,="" mg1655="" min="" nid:g1787156;="" ompf;="" pid:g17871="" pidn:aac74015.1;="" position:="" source:="" strain="" substrain="" td="" tolf;=""><td>A; Molecule type: DNA A; Molecule type: DNA A; Residues: 33-63 <nog> A; Residues: 33-63 <nog> A; Residues: D.J.; Mau, B.; Shao, Y. A; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12. A; Reference number: A64720; MUID:97426617 A; Accession: H64832</nog></nog></td><td>A;Accession: A90314 A;Mclecule type: protein A;Mclecule type: protein A;Residues: 23-87,'E',89-138,'G',140-283,'L',285-362 <che> A;Residues: 23-87,'E',89-138,'G',140-283,'L',285-362 <che> A;Residues: 23-87,'E',89-138,'G',140-283,'L',285-362 <che> A;Mizuno, T:, Mizunohima, S. J. Bacteriol: 164, 797-801, 1985 A;Title: Construction of a series of ompF-ompC chimeric genes by in vivo homologous r A;Reference number: A91809; MUID:86033642</che></che></che></td><td>A; Accession: A91301 A; Molecule type: DNA A; Mesidues: 1-37 <mut> R; Chen, R.; Kramer, C.; Schmidmayr, W.; Chen-Schmeisser, U.; Henning, U. Biochem. J. 203, 33-43, 1982 A; Title: Primary structure of major outer-membrane protein I (ompF protein, porin) of A; Reference number: A90314; MUID:82256494</mut></td><td>A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-362 <ino> A; Residues: 1-362 <ino> A; Cross-references: GB:J01655; GB:M10311; GB:M10312; NID:g147009; PIDN:AAA24244.1; PI A; Experimental source: strain K12 A; Experimental source: strain K12 R; Mutoh, N.; Inokuchi, K.; Mizushima, S. FEBS Lett. 137, 171-174, 1982 A; Title: Amino acid sequence of the signal peptide of OmpF, a major outer membrane pr A; Reference number: A91301; MUID:82139379</ino></ino></td><td>RESULT 1 MMECF outer membrane porin ompF precursor - Escherichia coli outer membrane porin ompF precursor - Escherichia coli N;Alternate names: outer membrane protein la; outer membrane protein b C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 13-Jun-1983 #text_change 16-Jul-1999 C;Accession: A93449; A91301; A90314; A25029; H64832; A03431 C;Accession: A93449; A91301; A90314; A25029; H64832; A03431 C;Accession: A93449; Muclei Asception: A93449; MUID:83090452 A:Accession: A93449; MUID:83090452</td></blats>	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 33-63 <nog> A; Residues: 33-63 <nog> A; Residues: D.J.; Mau, B.; Shao, Y. A; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12. A; Reference number: A64720; MUID:97426617 A; Accession: H64832</nog></nog>	A;Accession: A90314 A;Mclecule type: protein A;Mclecule type: protein A;Residues: 23-87,'E',89-138,'G',140-283,'L',285-362 <che> A;Residues: 23-87,'E',89-138,'G',140-283,'L',285-362 <che> A;Residues: 23-87,'E',89-138,'G',140-283,'L',285-362 <che> A;Mizuno, T:, Mizunohima, S. J. Bacteriol: 164, 797-801, 1985 A;Title: Construction of a series of ompF-ompC chimeric genes by in vivo homologous r A;Reference number: A91809; MUID:86033642</che></che></che>	A; Accession: A91301 A; Molecule type: DNA A; Mesidues: 1-37 <mut> R; Chen, R.; Kramer, C.; Schmidmayr, W.; Chen-Schmeisser, U.; Henning, U. Biochem. J. 203, 33-43, 1982 A; Title: Primary structure of major outer-membrane protein I (ompF protein, porin) of A; Reference number: A90314; MUID:82256494</mut>	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-362 <ino> A; Residues: 1-362 <ino> A; Cross-references: GB:J01655; GB:M10311; GB:M10312; NID:g147009; PIDN:AAA24244.1; PI A; Experimental source: strain K12 A; Experimental source: strain K12 R; Mutoh, N.; Inokuchi, K.; Mizushima, S. FEBS Lett. 137, 171-174, 1982 A; Title: Amino acid sequence of the signal peptide of OmpF, a major outer membrane pr A; Reference number: A91301; MUID:82139379</ino></ino>	RESULT 1 MMECF outer membrane porin ompF precursor - Escherichia coli outer membrane porin ompF precursor - Escherichia coli N;Alternate names: outer membrane protein la; outer membrane protein b C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 13-Jun-1983 #text_change 16-Jul-1999 C;Accession: A93449; A91301; A90314; A25029; H64832; A03431 C;Accession: A93449; A91301; A90314; A25029; H64832; A03431 C;Accession: A93449; Muclei Asception: A93449; MUID:83090452 A:Accession: A93449; MUID:83090452

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C; Function: <POR>
A; Description: forms aqueous channels that faciliate C; Function: <REC>
A; Description: receptor for bacteriophage T2
A; Description: receptor for bacteriophage T2
C; Superfamily: outer membrane protein phoE
C; Keywords: membrane protein; porin; trimer
F; 1-22/Domain: signal sequence #status predicted <SI
F; 23-362/Product: outer membrane porin ompF #status
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A; Residues: 1-362 <STO>
A; Cross references: GB: AE005174; NID: g12514104; PIDN: AAG55414.1;
A; Experimental source: strain O157: H7, substrain EDL933
C; Genetics:
A; Gene: compf
C; Superfamily: outer membrane protein phoE
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                                                    AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ
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Pred. No. 3e-123;
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A; Residues: 1-351 <STO>
A; Cross-references: GB:
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A; Accession: B85513
A; Status: preliminary
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iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.;
Nature 409, 529-533, 2001
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GATYYFNKNMSTYVDYIINQIDSDNKLGVGSDDTVAVGIVYQF 340
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GATYYFNKNMSAFVDYKINQLDSDNKLNINNDDIVAVGMTYQF 351
                                                                                                       TPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVDLVNYFEV
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                                                                                                                                                            YEYEG--FGIVGAYGAADRINLQEAQPLGNGKKAEQWATGLKYDANNIYLAANYGETRNA
                                                                                                                                                                                                               DSSAQTDNFMTKRASGLATYRNTDFFGVIDGLNLTLQYQGKNENRDVKKQNGDGFGTSLT
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213; Conserv
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                                                                        GB:AE005174; NID:g12513015; PIDN:AAG54566.1; GSPDB:GN00145; UWGP:
ce: strain 0157:H7, substrain EDL933
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Pred. No. 2.9e-73;
8; Mismatches 76;
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A.; Dimalanta, E.;
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#sequence_revision

Escherichia coli

13-Jun-1983 #text_change

21-Jul-2000

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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-351 <BLAT>
A;Cross references: GB:RE000132; GB:U00096; NID:g2367098; PIDN:AAC73345.1; PID:g1786436;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
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A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617
A;Accession: B64749
                                   outer membrane porin phoE precursor - (;Species: Citrobacter freundii C;Date: 20-Feb-1995 #sequence_revision C;Accession: $25520 R;Spierings, G.; Ockhuysen, C.; Hofstra
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A; Map position: 6 min
C; Complex: homotrimer
C; Function:
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submitted, to
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A; Residues: 1-351 < OVE>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVYYDALGYTDMLPEFGG 120
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the EMBL Data Library, August
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                                   Ockhuysen, C.; Hofstra, H.; Tommassen,
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Pred. No. 4.8e-73;
8; Mismatches 76
                                                                                                                                                                                             Citrobacter freundii
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A; Description: allows passive diffusion of small hyder, a; Note: induced under phosphate limitation C; Superfamily: outer membrane protein phoE C; Keywords: homotrimer; membrane protein; porin F;1-21/Domain: signal sequence #status predicted <SI F;22-351/Product: outer membrane porin phoE #status
A;Title: Characterization of the Salmonella typhimurium phoE gene and A;Reference number: JQ1937; MUID:93083994
A;Accession: JQ1937
                                                    A; Molecule type: DNA
A; Residues: 1-350 <SPI>
A; Cross-references: EMBL: X68023;
A; Cross-referentes: Extrain LT(
R; Spierings, G.; Elders, R.; van
Gene 122, 45-52, 1992
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                                                                                                                                                              A; Reference number: S25525
A; Accession: S25525
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C;Complex: homotrimer
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A; Accession: S25520
A; Molecule type: DNA
A; Residues: 1-351 <SPI>
                                                                                                                                                                                                  submitted to the EMBL Data Library, August
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Best Local :
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; Pred. No. 3.86
48; Mismatches
                                                                      Lith, B.;
                                                                                         NID:g47821; PIDN:CAA48164.1;
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                                                                        Hofstra,
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3.8e-70;
nes 76;
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A; Molecule type: DNA A; Residues: 1-197;199-350 <SP2> A; Cross-references: EMBL:X68023 A; Note: neither the full codon I

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Figure

A; Note: neither C; Genetics:

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A:Gene: phoE
C:Superfamily: outer membrane protein phoE
C:Keywords: membrane protein; porin; trimer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-330/Product: outer membrane porin phoE #status pre
                                                                                                                                                                                                                                                                 C;Superfamily: outer membrane protein phoE
C;Keywords: membrane protein; porin; trimer
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-365/Product: outer membrane porin lc #status pred
                                                                                                                                                                                                                                                                                                                                                                                               R;Blasband, A.J.; Marcotte Jr., W.R.; Schnaitman, C.A. J. Biol. Chem. 261, 12723-12732, 1986 A;Title: Structure of the lc and nmpC outer membrane porin A;Reference number: A25647; MUID:86304457 A;Accession: D25647
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C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
C;Accession: D25647
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A; Residues: 1-365 <BLA>
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;Superfamily: outer membrane protein phoE
                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: phage PAZ;Note: host Escherichia coli
                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                          Matches
   138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194
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                                                                                                                                                                                                           Local Similarity
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                                                                                                                                            1 AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ 60
                                                                              WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATYYFNKNMSTYVDYIINQIDSDNKLGVGSDDTVAVGIVYQF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEYEG--FGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAANYGETRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVDLVNYFEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DT-AYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNER---DTARRSNGDGVGG
                                                                                                                              AEIYNKDSNKLDLYGKVNAKHYFSSNDAD-----DGDTTYARLGFKGETQINDQLTGFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATYYFNKNMSAFVDYKINQLDSDNTLGINDDDIVAIGLTYQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPV-----SGGFANKTQNFEAVIQYQFDFGLRPSLGYVLSKGKDIEGVGSEDLVNYIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDFGGSDFAVSGAYTLSDRTREQNLQRRGTGDKAEAWATGVKYDANDIYIATFYSETRNM
                                                               WEYEFKGNRAE-SQGSSKDKTRLAFAGLKFGDYGSIDYGRNYGVAYDIGAWTDVLPEFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                         58.1%;
59.8%;
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                                                                                                                                                                                    Score 1051; Db ...
pred. No. 9.3e-69;
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Pred. No. 2.
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.8e-69;
                                                                                                                                                                                                                                                                      predicted <MAT>
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                                                                                                                                                                                          Indels 24;
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A;Description: one of the E. coli major outer membrane protein C;Superfamily: outer membrane protein phoE C;Keywords: membrane protein; portin; trimer F;1-21/Domain: Signal sequence #status predicted <SIG> F;22-367/Product: outer membrane porin ompC #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 32-57 <NOG>
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Pern
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Pern
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia
A; Reference number: A64720; MUID: 97426617
A; Accession: E64991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-40 <MI2>
A; Residues: 1-70 <MI2>
R; Nogami, T.; Mizushima, S.

J. Bacteriol. 164, 797-801, 1985
J. Fittle: Construction of a series of ompF-ompC chimeric A; Reference number: A91809; MUID:86033642
A; Accession: B25029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:K00541; GB:M10314; GB:M14188; R;Mizuno, T.; Chou, M.Y.; Inouye, M. FEBS Lett. 151, 159-164, 1983
A;Title: DNA sequence of the promoter region of the ca;Reference number: A18885; MUID:83132326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Mizuno, T.; Chou, M.Y.; Inouye, M.
J. Biol. Chem. 258, 6932-6940, 1983
A;Title: A comparative study on the genes
A;Reference number: A20867; MUID:83213433
A;Accession: A20867
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                                                                                                                                                                                                                                                               A; Map position: 47 min
                                                                                                                                                                                                                                                                                   C; Genetics:
A; Gene: ompC
                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-367 <BLAT>
A;Cross-references: GB:AE000310; GB:U00096; NID:g2367131; A;Experimental source: strain K-12, substrain MG1655
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                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A18885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-367 <MIZ>
                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVKYYDVGATYYFNKNMSTFVDYKINLLDKNDFTKALGVSTDDIVAVGLVYQF 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSETQNMTVFADHFV-----ANKAQNFEAVAQYQFDFGLRPSVAYLQSKGKDLGVWGDQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGETRNATPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SISYEYEGFGIVGAYGAADRTNLQE-----AQPLGNGKKAEQWATGLKYDANNIYLAAN
    Conservative
                      58.1%;
58.9%;
  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G.; Bloch, C.A.; Perna, N.T.; Y.
Score 1051; DB 1;
Pred. No. 9.4e-69;
5; Mismatches 69;
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                                            Length
                                                                                                                                                                                                                 proteins that form passive
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    Indels
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    8;
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AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ

-DNKDVDGDQTYMRLGFKGETQVTDQLTGYGQ

WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG

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A.Description: allows passive diffusion of small hydrophilic molecules with molecular we A.Note: induced under phosphate limitation C.Superfamily: outer membrane protein phoE C.Keywords: membrane protein; porin F.1-20/Domain: signal sequence *status predicted <SIG> F.21-350/Product: outer membrane porin phoE *status predicted <OPP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Experimental source: isolate IMSS-1
A;Note: this is one of the proteins induced when the E. d compounds, and some other negatively charged solutes C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outer membrane porin phoE precursor - Salmonella typhi
C;Species: Salmonella typhi
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #te
C;Accession: S36606
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C; Complex: homotrimer
C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-350 < TOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S36606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Torres, A.; Puente, J.L.; Calva, I submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                           1 AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDFGGSDFAVSGAYTLSDRTREQNLQRRGTGDKAEGWATGVKYDANDIYIATFYSETRNM
                                                                                                       YEYEG--FGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAANYGETRNA
                                                                                                                                             DSSAQTDNEMTKRASGLATYRNTDEFGIVDGLDLTLQYQGKNEDRDVKKQNGDGFGTSVS
                                                                                                                                                                                                                    WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYDDEDILKYVDVGATYYFNKNMSTYVDYKINLLD-DNQFTRDAGINTDNIVALGLVYQF
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                                                        TPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVDLVNYFEV
                                                                                                                                                                        D-TAYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNERDTARRSNGDGVGGSIS
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                                                                                                                                                                                                                                                               AEVYNKNGNKLDVYGKVKAMHYMSDYDSK-----DGDQSYVRFGFKGKTQINDQLTGYGR 75
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                                                                                                                                                                                                                                                                                                                          197;
                                                                                                                                                                                                                                                                                                                        Conservative
                            SGGFANKTQNFEAVIQYQFDFGLRPSLGYVLSKGKDIEGVGSEDLVNYIDV
                                                                                                                                                                                                                                                                                                                                      57.7%;
57.4%;
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                                                                                                                                                                                                                                                                                                                                    Score 1044; DB 2;
Pred. No. 2.8e-68;
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                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                  Length 350;
                                                                                                                                                                                                                                                                                                                        Indels 16;
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                                                                                                                                                                                                                                                                                                                       Gaps
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Db 308 GAIYYENKNMSAFYDYKINQLDSDNTLGINDDDIVAIGLTYQF 350
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onter membrane porin nmpC precursor - Escherichia coli cryptic lambdoid prophage DLP1 c.) Species: Escherichia coli c.) Species: Isocherichia coli c.) Species: Isocherichia coli c.) Species: S
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YSETQNMTVFADHFV--
                                                             YGETRNATPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVD 290
                                                                                                                                  SATYEYEGFGIGATYAKSDRTDTQVNAGKVLPEVFASGKNAEVWAAGLKYDANNIYLATT
                                                                                                                                                                          SISYEYEGFGIVGAYGAADRTNLQE-----AQPLGNGKKAEQWATGLKYDANNIYLAAN
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-ANKAQNFEAVAQYQFDFGLRPSVAYLQSKGKDLGVWGDQD
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Pred. No. 4.2e-68;
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C;Accession: B85861
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; F R;Perna, N.T.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou Nature 409, 529-533, 2001
Nature 409, 529-533, 2001
N;Title: Genome sequence of enterophemorrhagic Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74459.1; A;Experimental source: strain K-12, substrain MG1655 C;Superfamily: outer membrane prottein phrE C;Keywords: membrane prottein; trimer C;Keywords: membrane prottein; por1n; trimer E;1-21/Domain: signal sequence #status predicted <SIG> F;22-377/Product: probable outer membrane porin bl377 #status predicted <OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: D64888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     outer membrane porin b1377 precursor - Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 20-Aug-1999
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                                                                                                                                                     outer membrane protein 1b (Ibc) [imported] - Escherichia coli (strain 0157:H7) C;Species: Escherichia coli (C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
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A; Residues: 1-377 <BLAT>
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A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Accession: B85861
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LVKYVDVGATYYEKKNMSTEVDYKINLLDKNDETKALGVSTDDIVAVGLVYQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GIGDVDLVNYFEVGATYYFNKNMSTYVDYIINQIDSDNKL----GVGSDDTVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEYNIQANNTESSKNQSW--TRLAFAGLKFADYGSFDYGRNYGVMYDIEGWTDMLPEFGG
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Pred. No. 1.4e-67;
2; Mismatches 78;
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                                                                                          D.J.;
K.; A
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: CNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross references: GB:AE005174; NID:g12516550; PIDN:AAG57350.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                R;Alberti, S.
R;Alberti, S.
submitted to the EMBL Data Library, May 1994
submitted to The EMBL Data Library, May 1994
                                                                                                                                  C;Superfamily: outer membrane protein phoE
C;Keywords: membrane protein; brin; trimer
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-363/Product: outer membrane porin ompK36 #status predicted
                                                                                                                                                                                                                                                                                                                                                     C;Species: Klebsiella pneumoniae
C;Date: 07-May-1995 #sequence_revision
C;Accession: S51104
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
S51104
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C;Superfamily: outer membrane protein
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A; Accession: S51104
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A; Residues: 1-363 <ALB>
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 22
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AEIYNKDGNKLDLYGKIDGLHYFS---
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58.7%;
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Pred. No. 1.9e
43; Mismatches
                                                          Score 1030; DB Pred. No. 3e-67; Mismatches
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 -DDKDVDGDQTYMRLGVKGETQINDQLTGYGQ
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1.9e-67;
                                                                                       DB 2;
                                                                                                                                                                                                                                PIDN:CAA83913.1;
                                                              82;
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A; Molecule type: DNA
A; Residues: 1-363 <VENN
A; Residues: 1-363 <VENN
A; Cross-references: EMBL: Z31594; NID: g468740; PIDN: CAA83471.1; PID: g
C; Genetics:
C; Genetics:
C; Superfamily: Outer membrane protein phoE
C; Keywords: membrane protein; porin; trimer
C; Keywords: membrane protein; porin; trimer
F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 23-363/Product: outer membrane porin ompF #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Venegas, A.; Gomez, I.; Bruce, E.; Martinez, M. submitted to the EMBL Data Library, March 1994 A:Description: PCR amplification and cloning of the A;Reference number: $43159 A:Accession: $43159
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 317
            296 EVGATYYFNKNMSTYVDYIINQIDSDNKLG--VGSDDTVAVGIVYQF 340
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                                                                                                                                                                                                                                                                                                                      1 AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ
                                                                                                                                SISYEYEGFGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAANYGETRN
                                                                                                                                                                                          DT---AYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNERDTARRS-NGDGVGG 176
                                                                       ATPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGI-GDVDLVNYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QYTQTYNATR-----AGSLGFANKAQNFEVAAQYQFDFGLRPSVAYLQSKGKDLNGYGDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTAYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKN-----ERDT-----ARRSN 170
QAGATYYFNKNMVWVDYRFNLLDENDYSSSYVGTDDQAAVGIVYQF
                                                        MSIVENTVTDTVEMANKTQNLEVVAQYQFDFGLRPAISYVQSKGKQLNGAGGSADLAKYI
                                                                                                                                                                                                                                                 WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG
                                                                                                                                                                                                                                                                                         GDGFGTSVTYDIFDGISAGFAYANSKRTDDQNQLLLGEGDHAETYTGGLKYDANNIYLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDGVGGSISYE-YEGFGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMAYEFDGFGVTAAYSNSKRTNDQQDRD-GNGDRAASWAVGAKYDANNVYLAAVYAETRN
                                                                                                                                                                         ETWGGAYTDNYMTSRAGGLLTYRNSDFFGLVDGLSFGIQYQGKNQDNHSINSQNGDGVGY 197
                                                                                                                                                                                                                                    WEYRTKADRAEG-EQQNSNLVRLAFAGLKYAEVGSIDYGRNYGIVYDVESYTDMAPYFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DILKYVDVGATYYFNKNMSTYVDYKINLLDDNSFTRSAGISTDDVVALGLVYQF 363
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                   56.98;
                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                                                                                 Score 1029.5; DB 2;
Pred. No. 3.3e-67;
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A;Map position: 45 min
C;Superfamily: outer membrane protein phoE
C;Keywords: membrane protein; porin; trimer
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-378/Product: outer membrane porin ompC #status pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Venegas, A. submitted to the EMBL Data Library, submitted to the EMBL Data Library, submitted number: S10122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Venegas, A.; Gomez, I.; Zaror, I.; Yudelevich, A. Nucleic Acids Res. 16, 7721, 1988
A;Title: The nucleotide sequence of the Salmonella typhi A; Reference number: S01248; MUID:88319959
A; Accession: S01248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 outer membrane porin ompC precursor - Salmonella typhi
C;Species: Salmonella typhi
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: JQ0119; S01248; S10122
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A; Residues: 1-361,363-378 < VEN2>
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A;Residues: 1-5,'Q',7-361,363-378 <VEN1>
A;Cross-references: EMBL:X07835; NID:947796; PIDN:CAA30688.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-378 < PUE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 83, 197-206, 1989
A;Title: Comparative analysis of the Salmonella typhi and Escherichia coli ompC genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Puente, J.L.; Alvarez-Scherer, V.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M31424; NID:g154207; PIDN:AAA27169.1; R;Venegas, A.; Gomez, I.; Zaror, I.; Yudelevich, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 209;
                                                                                                                                                                                                                                                                        173
                                                                                                                                                                                                                                                                                                        194 GYGGSLTYAIGEGFSVGGAITTSKRTADQNNTANARLYGNGDRATVYTGGLKYDANNIYL
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                                    IVYQF 340
                                                                                                                                                                                                                                                       GVGGSISYEY-EGFGIVGAY----GAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYL
                                                                                                                                                                                                                                                                                                                                                                                                           WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG
LVYQF
                                                                            SNGYGASYGDQDIVKYVDVGATYYFNKNMSTYVDYKINLLDKNDFTRDAGINTDDIVALG
                                                                                                  E----GIGDVDLVNYFEVGATYYFNKNMSTYVDYIINQIDSDN----KLGVGSDDTVAVG
                                                                                                                                                                           AEIYNKDGNKLDLFGKVDGLHYFS-----DDKGSDGDQTYMRIGFKGETQVNDQLTGYGQ
                                                                                                                                                       AAQYSQTYNATRFGTSNGSNPSTSYGFANKAQNFEVVAQYQFDFGLRPSVAYLQSKGKDI
                                                                                                                                                                                                                                                                                                                                                                                         WEYQIQGNQTEGSN---DSWTRVAFAGLKFADAGSFDYGRNYGVTYDVTSWTDVLPEFGG
378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.6%;
57.3%;
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RESULT

Job time: 371 sec

Page 8

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Run
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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       Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     Score
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length:
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1809
1 AEIYNKDGNKVDLY
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         July 3, 2001, 15:10:50; Search time 37.35 Seconds (without alignments) 312.748 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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033980 serratia ma
q011605 citrobacter
p30705 salmonella
p06996 escherichia
p06996 escherichia
p07038 bacteriopha
q56619 salmonella
p071238 bacterichia
q011606 klebsiella
p77747 escherichia
q056113 salmonella
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p3732 salmonella
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p37335 escherichia
q054671 salmonella
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SEQUENCE OF 23-362. SEQUENCE OF 23-362. MEDLINE-82256494; PubMed-7049161; Chen R., Kramer C., Schmidmayr W., Chen-Schmeisser U., Henning U.;	Muton N., Inokuchi K., Mizushima SI.; "Amino acid sequence of the signal peptide of CmpF, a major outer membrane protein of Escherichia coli."; FEBS Lett. 137:171-174(1982).	[4] SEQUENCE OF 1-37 FROM N.A. MEDLINE-82139379; PubMed=7037455;	Yano M., Horiuchi T.: "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).	Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,	STRAIN=K12; MEDLINE=97061202; PubMed=8905232; MEDLINE=97061202; PubMed=8905232; Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,	Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997). [3] SEQUENCE FROM N.A.	STRAIN=K12 / MG1655; MEDLINE=97426617; Pubbed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,	"Primary structure of the ompr gene that codes for a major outer membrane protein of Escherichia coli K-12."; Nucleic Acids Res. 10:6957-6968(1982). [2] [2] SEQUENCE FROM N.A.

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1- FUNCTION: OMPF IS A PORIN THAT PASSIVE DIFFUSION PORES WHICH SMALL MOLECULAR WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE. IT IS ALSO RECEPTOR FOR THE BACTERIOPHAGE T2.

1- SUBUNIT: HOMOTRIMER.

1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRA.

1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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STRAIN-K12 / EMG2:
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MEDLINE-95024177; PubMed-7524100;
Jeanteur D., Schirmer T., Fourel D., Simonet V., Rummel G., Widmer C.

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MEDLINE-98291876; PubMed=9629924;
MO110y M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M.,
Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;
"Extraction of membrane proteins by differential solubilization
separation using two-dimensional gel electrophoresis.";
Electrophoresis 19:837-844(1998).
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MEDLINE-97443975; PubMed-9298646;
Link A.J., Robison K., Church G.M.;
Link A.J., Robison K., Church G.M.;
Comparing the predicted and observed properties
in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
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MEDLINE-86033642; PubMed-2997131;

MEDLINE-86033642; PubMed-2997131;

MOZDANI T., Mizushima S.;

"Construction of a series of ompF-ompC chimeric genes by in vivo of a series of ompF-ompC chimeric genes by in vivo of the translational products.";

The Bacteriol 164:797-801(1985).
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MEDLINE-99060042; PubMed-9843370;
Phale P.S., Philippsen A., Kiefhaber T
Schirmer T., Rosenbusch J.P.;
Stability of trimeric OmpF porin: the
                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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MEDLINE-92375189; PubMed=1380671;
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D90730; BAA35675.1; -
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   of Escherichia coli B/r.";
m. J. 203:33-43(1982).
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SERAIN-K12 / MC1655;
STRAIN-K12 / MC1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burl:
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
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Riley M., Collado-Vides J., Glasner J.D., Goeden M.A., Rose E
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STRAIN-KIZ / W3110;

STRAIN-KIZ / W3110;

Takemoto K., Mori H., Miki T., Hatada E., Fukuda R., Ichihara : Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara : Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.;

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4.0 - 6.0 min (189,987 - 281,416pp) region.";
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P02932;
21-JUL-1986
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PDB; 1PHO; 31-OCT-93.
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SWISS-2DPAGE; P02932; COLI.
ECOZDBASE; B037.0; 6TH EDITION.
ECOGENE; EG10729; phoE.
InterPro; IPR001897; -.
InterPro; IPR001897; -.
InterPro; IPR001897; -.
INTERPRO; IPR00183; ECOLINEIPORIN.
PRINTS; PR00182; ECOLINEIPORIN.
PRINTS; PR00183; ECOLIPORIN.
PROSITE; PS00576; GRAM, NEG_PORIN; 1.
Outer membrane; Transmembrane; Porir

Porin;

Signal;

3D-structure

PIR; A03432; MMECPE. PDB; 1PHO; 31-OCT-93.

EMBL;

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TOPOLOGY.

MEDLINE-93172954; PubMed-7679770;

Struyve M., Visser J., Adriaanse H., Benz R., Tommassen J.;

Struyve M., Visser J., Adriaanse H., Benz R., Tommassen J.;

"Topology of PhoE porin: the 'eyelet' region.";

Mol. Microbiol. 7:131-140(1993).

Mol. Microbiol. 7:131-140(1993).

INDUCED WHEN E.COLI CE
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PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE,
PARTICULARLY EFFICIENT IN THE UPT
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MEDLINE=92375189; PubMed=1380671;
Cowan S.W., Schirmer T., Rummel G., Ste
Pauptit R.A., Jansonius J.N., Rosenbuse
"Crystal structures explain functional
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Nucleic Acids Res. 12:6337-6355(1984).
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Lashkari D., Lew H.,
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h A., Oefner
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R PROSITE; PS00576; GRAM_NEC_PORIN; 1.

PR PROSITE; PS00576; GRAM_NEC_PORIN; 1.

PR PROSITE; PS00576; GRAM_NEC_PORIN; 1.

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                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001702; -.
InterPro; IPR001897; -.
Pfam; PF00267; Gram-ve_porins;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
                                                                                                                                                                                              AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ 60
 TPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVDLVNYFEV
                                                                          WEYNFOGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEEGG 120
                                                                                                                                                                             AEVYNKNGNKLDVYGKVKAMHYISDDDTK-----DGDQTYVRFGFKGETQINDQLTGYGR
                         YEYEG--FGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAANYGETRNA
                                                                                                                              WEAEFAGNKAESDSSQ----KTRLAFAGLKLKDFGSLDYGRNLGALYDVEAWTDMFPEFGG
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207; Conser
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(Rel.
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                                                                                                                                                                                                                                              59.3%;
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                                                                                                                                                                                                                                  Pred. No. 1.8); Mismatches
                                                                                                                                                                                                                                                            Score 1072.5;
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Best Local Similarity
Matches 215; Conserv
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SEQUENCE
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PRINTS; PR00183; ECCLIPORIN.
PROSITE; PS00576; GRAM_NEG_PORIN; 1.
Outer membrane; Transmembrane; Porin; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hutsul J.A.M., Worobec E.A.;

"Molecular characterization of the Serratia marcescens OmpF porin, and analysis of S. marcescens OmpF and OmpC osmoregulation.";

Microbiology 143:797-2806(1997).

-i- SUBUNIT: HONOTRINER (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.

-i- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF).
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                                                                         DT-AYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNERD--TARRSNGDGVGGS
                                                                                                                                                                                                        AETYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ
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STYDIGEGVSFGAAYASSNRTDDQKLRSNERGDKADAWTVGAKYDANNVYLAAMYAETRN
               DTYTYSDNFMTGRTNGVATYRNNNFFGLVDGLNFALQYQGKNQNDGRDVKKQNGDGWGIS
                                                                                                                  WEYNVQSNHAESQGTE-GTKTRLGFAGLKFADYGSFDYGRNYGVLYDVEGWTDMLPEFGG
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374 AA;
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Pred. No. 2.
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OUTER MEMBRANE PROTEIN F.
BF821D385E441049 CRC64;
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InterPro; IPH001877; ...
InterPro; IPR001897; ...
Pfam; PF00267; Gram ve_porins; 1.
PRINTS; PR00182; ECOLNEIPORIN.
PRINTS; PR00183; ECOLIPORIN.
PROSITE; PS00576; GRAM_NEG_PORIN; 1.
Outer membrane; Transmembrane; Porin; Signal.
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MEDLINE=93146376; PubMed=1337052;

MEDLINE=93146376; PubMed=1337052;

Spierings G., Ockhuijsen C., Hofstra H., Tommassen J.;

"Characterization of the Citrobacter freundii phoE gene and development of C. freundii-specific oligonucleotides.";

FEMS Microbiol. Lett. 78:199-204(1992).

-!- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN CELLS ARE GROWN UNDER PHOSPHATE LIMITATION. TIS PROTEIN PORE IS PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE, PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOLUTES:
-!- SUBUNIT: HOMOTRIMER.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
-!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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77
                             61 WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG
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WEAEFAGNKAESDSNQ--QKTRLAFAGSKLKNLGSFDYGRNLGALYDVEAWTDMFPEFGG
                                                                                                                 AEVYNKNGNKLDLYGKVKAMHYMTDYDSK-----DGDQSYIRLGFKGETQINDELTGYGR
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351 (
38807 MW;
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Pred. No. 2.7e-69;
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01-APR-1993 (Rel. 25, Created)

01-APR-1993 (Rel. 25, Last sequence update)

15-DEC-1998 (Rel. 37, Last annotation updat

OUTER MEMBRANE PORE PROTEIN E PRECURSOR.
                                                                               StyGene; SG10291; phoE.
InterPro; IPR001702; -.
InterPro; IPR001897; -.
Pfam; PF00267; Gram-ve_porins; 1.
PRINTS; PR00182; ECOLIPERIN.
PRINTS; PR00183; ECOLIPERIN.
PROSITE; PS00576; GRAM_NGC_PORIN; 1.
Outer membrane; Transmembrane; Porin; Signal.
                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           Splerings G., Elders R., van Lith B., Hofstra H., Tommassen J.;

"Characterization of the Salmonella typhimurium phoE gene and
development of Salmonella-specific DNA probes.";

Gene 122:45-52(1992).

-I- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN CELLS ARE
GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE IS

PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE,
PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella typhimurium.
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PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93083994; PubMed-1280609;
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                                                                                                                                                                                                                                                                                                                                                                    SOLUTES.
SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
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P06996;
                               MEDLINE-97251358; PubMed-9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura Makino K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; Takemoto K., Wada C., Yamamoto Y., Horiuchi T., Yamamoto Y., Yamamoto
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MEDLINE-83213433; PubMed-6304064;
Mizuno T., Chou M.-Y., Inouye M.;
"A comparative study on the genes for thr
coll outer membrane. DNA sequence of the
J. Biol. Chem. 258:6932-6940(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence of Escherichia coli K-12.", nce 277:1453-1474(1997).
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(Rel. 07, Last sequence update)
(Rel. 40, Last annotation updat)
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Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M., Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.; "Extraction of membrane proteins by differential solubilization separation using two-dimensional gel electrophoresis."; Electrophoresis 19:837-844(1998).

-I- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOI WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
                                                                                                                                                                                                                     EMBL; K00541; AAA24243.1; -.
EMBL; AE000310; AAC75275.1; -.
EMBL; D90850; BAA15998.1; -.
EMBL; U00008; AAA16412.1; -.
PIR; A20867; MMECPC.
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STRAIN-K12 / W3110
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MEDLINE-97443975; PubMed-9298646;
Link A.J., Robison K., Church G.M.;
Linkparing the predicted and observed properties of proteins in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
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"DNA sequence of the promoter region
acid sequence of the signal peptide (
Escherichia coll.";
                                                           PRINTS: PR00182: ECOLNEIPORIN.
PRINTS: PR00183: ECOLIPORIN.
PROSITE: PS00576: GRAM_NEG_PORIN;
                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                Outer membrane;
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MEDLINE-98291876; PubMed-9629924;
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SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS
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164:797-801(1985).
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Best Local Similarity
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P30704;
01-APR-1993
01-APR-1993
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                       species. Implications for structure-function relationships in a pore-forming protein of the outer membrane.";
EUR. J. BLOCHEM. 164:469-475(1987).

-I: FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN CELLS ARIGNAM UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE IS PARTICULARLY EFFICIENT IN THE UPPARE OF INORGANIC PHOSPHATE. PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED
                                                                                                                                                                                          between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There
use by non-profit institutions as long as a
modified and this statement is not removed. Us
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"A comparative study on the phoE genes of three."
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                                                                                                                                               an email to license@isb-sib.ch).
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(Rel. 25, Last sequence update)
(Rel. 37, Last annotation updat
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InterPro; InterPro;

IPR001702; -. IPR001897; -.

Gram-ve_porins;

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JR PRINTS; PRO0183; ECOLIPORIN.

DR PROSTIE; PS00576; GRAM_NEG_PORIN; 1.

Outer membrane; Transmembrane; Porin; Signal.

21 BY SIMILARITY.

OUTER MEMBRANE PORE PROTEIN E.

OUTER MEMBRANE PORE PROTEIN E.
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PO7238;
01-APR-1988
01-APR-1988
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between
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MEDLINE-86304457; PubMed-3017988;
Blasband A.J., Marcotte W.R. Jr., Schnaitman
"Structure of the lc and nmpC outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                         lambdoid bacteriophage.";
J. Biol. Chem. 261:12723-12732(1986).
I- FUNCTION: PORINS ARE MAJOR PROTEINS FOUND OF GRAM-NEGATIVE BACTERIA WHERE THEY FORM NONSPECIFIC PERMEATION OF SMALL SOLUTES (NOT THE PROPERTY OF THE PROPER
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MISCELLANEOUS: A PORIN GENE CAN ALSO BE FOUND IN THE GENTAIN LAMBDOID BACTERIOPHAGE, AND ITS PROTEIN IS EXE THE LYSOGENIC STATE. IN E.COLI THE EXPRESSION OF OMPC PROTEINS IS THEN REDUCED SUBSTATIFILLY.
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SUBUNIT: HOMOTRIMER (BY SIMILARITY)
SUBCELLULAR LOCATION: INTEGRAL MEMB
                                                                                                                                  SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS
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                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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(Rel. 07, Last sequence update)
(Rel. 37, Last annotation update)
ANE PORIN PROTEIN LC PRECURSOR.
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Best Local Similarity
Matches 210; Conserv
    STRAIN=IMSS-1;
TOTICS A., Puente J.L., Calva E.;
TOTICS A., Puente J.L., Calva E.;
Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN (
GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE
PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC P
                                                                                                                                                                                                                                                                                                                                                                                 Q56119;
01-NOV-1997
01-NOV-1997
15-DEC-1998
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                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Salmonella.
                                                                                                                                                                                                                                                                                                            PHOE.
Salmonella typhi
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                                                                                                                                                                                         SEQUENCE FROM N.A.
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InterPro; IPR001897; -.
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D25647; MMBPP2.
  PHOSPHORYLATED SOLUTES.
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annotation update)
N E PRECURSOR.
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Pred. No. 1
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H -> R (IN AA SEQUENCE).
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OFBC0531FB9C0205 CRC64;
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InterPro; IPKUV--.

( Pfam; PF00267; Gram-Ve_PV--.

R PRINTS; PR00182; ECOLNEIPORIN.

R PRINTS; PR00183; ECOLLPORIN; 1.

PR PROSTTE; PS00576; GRAM_NEC_PORIN; 1.

Outer membrane; Transmembrane; Porin; Signal.

KW Outer membrane; Transmembrane; Porin; Signal.

OUTER MEMBRANE PORE PROTEIN E.

OUTER MEMBRANE PORE PROTEIN E.

OUTER MEMBRANE PORE PROTEIN E.
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Best Local Similarity
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                                                                                                                                  P21420; P77189;
P21420; P77189;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                              NMPC_ECOLI
SEQUENCE FROM N.A.
STRAIN-MUTANT CS384;
MEDLINE-86304457; PubMed-3017988;
Blasband A.J., Marcotte W.R. Jr.,
                                                                                                       Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001702; -.
InterPro; IPR001897; -.
Pfam; PF00267; Gram-ve_porins;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -I- SUBUNIT: HOMOTRIMER.
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
-I- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
                                                                                                                                                                                                                                                                                                           308
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STRAIN=K12 / MG1655;
MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
Mau B., Shao Y.;
                                        Pfam; PF00267; Gram-ve_porins; 1.
PRINTS; PR00182; ECOLNEIPORIN.
PRINTS; PR00183; ECOLIPORIN.
PROSITE; PS00576; GRAM_NEG_PORIN; 1.
Outer membrane; Transmembrane; Porin; SIGNAL
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                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94335635; PubMed-8057841;
Coll J.L., Heyde M., Portalier R.;
Cerrange of the nmpC gene of Escherichia coli K-12 is modulated external pH. Identification of cis-acting regulatory sequences involved in this regulation.";
Mol. Microbiol. 12:83-93(1994).
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EMBL; U82598; AAB40749.1; ALT_SEQ.

EMBL; 235442; CAA64594.1; -.

EMBL; X92587; CAA63325.1; -.

PIR; A25647; MMECNC.
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                             CHAIN
                                                                                                                           HSSP; P02931; 1GFN.
EcoGene; EG10659; nmpC.
InterPro; IPR001702; -.
InterPro; IPR001897; -.
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Chem. 261:12723-12732(1986).
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OUTER MEMBRANE PORIN PROTEIN NMPC.
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01-APR-1993
15-DEC-1998
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Spierings G., Ockhuijsen C., Hofstra H., Tommassen J.;

Spierings G., Ockhuijsen C., Hofstra H., Tommassen J.;

Spierings G., Ockhuijsen C., Hofstra H., Tommassen J.;

"Characterization of the Citrobacter freundii phoE gene and development of C. freundii-specific oligonucleotides.";

FEMS Microbiol. Lett. 78:199-204(1992).

1- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN CELLS ARE GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE IS PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE, PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED
                                                                                                                       the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                  InterPro; IPR001702;
InterPro; IPR001897;
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SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER
SUBCELLULAR LOCATION: THE OMPC/PHOE FAMILY OF PORINS.
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Alba H., Rashimoto K., Kimaysshi K., Inada T., Isono K., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura I., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Sigampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yanamoto Y., Horluchi T., Takemoto K., Takeuchi Y., Wada C., Yanamoto Y., Horluchi T., A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map. DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE-91426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna Blattner F.R., Plunkett G. III, Bloch C.A., Perna Riley M., Collado-Vides J., Glasner J.D., Rode C.
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Bacteria; Proteobacteria;
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15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
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43; Mismatches
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InterPro; IPR001702; -
InterPro; IPR001897; -
InterPro; IPR001897; -
Pfam; PF00267; Gram-ve_porins; 1
PRINTS; PR00182; ECOLNEIPORIN.
PRINTS; PR00183; ECOLIPORIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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377 AA;
(Rel. 37, Created)
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Pred. No. 9e-67;
2; Mismatches 78;
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InterPro; IPR001897; ...
Pfam; PF00267; Gram-ve_porins; 1.
PRINTS; PR00182; ECOLMEIPORIN.
PRINTS; PR00183; ECOLMEIRORIN.
1.
PROSITE; PS00576; GRAM_NEG_PORIN; 1.
Outer membrane; Transmembrane; Porin; Phage recognition; Outer membrane; Transmembrane; Porin; Phage recognition; SIGNAL 1 22 BY SIMILARITY.
SIGNAL 1 23 363 OUTER MEMBRANE PROTEIN F.
CHAIN 23 363 FORESTER PROTEIN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fernandez-Mora M., Calva E.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: OMPE IS A PORIN THAT PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE. IT IS ALSO RECEPTOR FOR THE BACTERIOPHAGE T2 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella typhi.
Bacteria; Proteobacteria;
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15-DEC-1998 (Rel. 37, Last annotation update)
OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF)
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QAGATYYFNKNMNVWVDYRFNLLDENDYSSSYVGTDDQAAVGITYQF
                                                                  MSIVENTVTDTVEMANKTQNLEVVAQYQFDFGLRPAISYVQSKGKQLNGAGGSADLAKYI
                                                                                  TMAYEFDGFGVTAAYSNSKRTNDQQDRD-GNGDRAESWAVGAKYDANNVYLAAVYAETRN
                                                                                                                                                        SISYEYEGFGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAANYGETRN
                                                                                                                                                                                                    ETWGGAYTDNYMTSRAGGLLTYRNSDFFGLVDGLSFGIQYQGKNQDNHSINSQNGDGVGY
                                                                                                                                                                                                                        DT---AYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNERDTARRS-NGDGVGG
                                                                                                                                                                                                                                                                       WEYRTKADRAEG-EQQNSNLVRLAFAGLKYAEVGSIDYGRNYGIVYDVESYTDMAPYFSG
                                                                                                                                                                                                                                                                                       WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG
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57.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dutzler R., Rummel G., Alberti S., Hernandez-Alles S., Phale P.S., Rosenbusch J.P., Benedi V.J., Schirmer T.;
"Crystal structure and functional characterization of OmpK36, the osmoporin of Klebsiella pneumoniae.";
Structure 7:425-434(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 i5-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMPC) (PORIN OMPK36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosenbusch J.P., Benedi V.J.;
"A porin from Klebsiella pneumoniae: sequence homology, three-dimensional model, and complement binding.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
MEDLINE-99216538; PubMed-10196126;
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                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                  PROSITE; PS00576; GRAM_NEG_PORIN; 1.
Outer membrane; Transmembrane; Porin; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00182; ECOLNEIPORIN. PRINTS; PR00183; ECOLIPORIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z33506; CAA83913.1; -.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE. IN K.PNEUMONLAE IT HAS BEEN SHOWN TO BIND C10 COMPONENT AND ACTIVATE THE CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM.
DTAYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKN-----ERDT-----ARRSN 170
                                                                    WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG 120
                                                 WEYNVQANNTESSSDQAW--TRLAFAGLKFGDAGSFDYGRNYGVVYDVTSWTDVLPEFGG
                                                                                                                  AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ 60
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IPR001702; -.
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Pred. No. 2e-6
37; Mismatches
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                   DLVNYFEVGATYYFNKNMSTYVDYIINQIDSDN---KLGVGSDDTVAVGIVYQF 340
                                                                 QYTQTYNATR----AGSLGFANKAQNFEVAAQYQFDFGLRPSVAYLQSKGKDLNGYGDQ
                                                                                    NYGETRNATPITNKFTNTSGFANKTQDVLLVAQYQEDFGLRPSIAYTKSKAKDVEGIGDV
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                                                                                                                                                                  GDGVGGSISYE-YEGFGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAA
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DILKYVDVGATYYFNKNMSTYVDYKINLLDDNSFTRSAGISTDDVVALGLVYQF 363
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                           085030 escherichia

09k597 escherichia

09k3e6 salmonella

09rh85 escherichia

09raw3 klebsiella

09raw3 klebsiella

09k3e7 salmonella

09k759 calymmatoba

09k759 calymmatoba

09k753 klebsiella

09f889 salmonella

09f889 salmonella

09c715 klebsiella

09c71 yersinia pe

052641 rahnella aq

094857 klebsiella
                                                                                                                                                                                       087754 klebsiella
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       5 escherichia
3 klebsiella
2 klebsiella
7 salmonella
9 calymmatoba
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1 yersinia pe
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Q9x587	066062	Q51266	054349	054347	070078	054340	P72113	051947	054344	P72072	054343	Q51273	Q9zc72	Q45106	066067	Q9x586	054345	054339	Q9r2d4	054350	P76871	P94743	Q9kku2	P77519	Q9rnal
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                                                                                                                                                                                                                                                                                                SIGNAL
CHAIN
SEQUENCE
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"Identification and characterization of a novel porin of Klebsiella pneumoniae: its role in beta-lactam antibiotics resistance."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ011502; CAA09666.1; -.
HSSP; Q48473; 10SM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000408; -.
InterPro; IPR001702; -.
Pfam: PF00267; Gram-ve_porins; 1.
PRINTS; PR00182; ECOLNEIPORIN.
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                                   1 AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ 60
AEIYNKDGNKLDLYGKVDGLHYFSSDSKK-----DGDQTYLRFGFKGETQINDILTGYGQ
                                                                                                                                                                 Similarity
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374 AA;
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374 O
41612 MW;
                                                                                                                              57.7%; Score 1044.5; DB 2; Length 58.5%; Pred. No. 9.3e-69; Live 37; Mismatches 76; Indels
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Best Local Similarity
Matches 210; Conser
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STRAIN-BE (BL21);

MEDLINE-98317278; PubMed-9642192;

MEDLINE-98317278; PubMed-9642192;

MILLON A., Phale P.S., Koebnik R., Widmer C.

"Identification and characterization of two quentification and characterization of two quentification in Escherichia coli BE.";

J. Bacteriol. 180:3388-3392(1998).

EMBL; AF035618; AAC38644.1; -...

HSSP; P02931; 1GFN.
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01-MAR-2001
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085030;
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InterPro; IPR001702; -.
Pfam; PF00267; Gram-ve_porins; 1.
PRINTS; PR00182; ECOLMEIPORIN.
PROSITE; PS00626; RCC1_2; UNKNOWN_1.
SEQUENCE 377 AA; 41236 MM; 7F4D6
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Escherichia.
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                                                                    DT-AYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNE----
                                                                                                                                       WEYNIQANNTESSKNQSW--TRLAFAGLKFADYGSFDYGRNYGVMYDIEGWTDMLPEFGG
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  RSNGDGVGGSISYEY-EGFGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIY 226
                                               DSYTNADNEMTGRANGVATYRNTDEFGLVNGLNEAVQYQGNNEGASNGQEGTNNGRD-VR
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Last sequence update)
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Pred. No. 3.9e-68;
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Matches 209
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01-OCT-2000 (TremBLrel. 15, C)
01-OCT-2000 (TremBLrel. 16, L
01-MAR-2001 (TremBLrel. 16, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPKUUUVU...
InterPro; IPRUUI702; -.
InterPro; IPRUUI702; -.
PERINTS; PROU1926; GRAM_NEG_PORIN; 1.
PROSITE; PSU0576; GRAM_NEG_PORIN; 1.
PROSITE; PSU0030; RNP_1; UNKNOWN 1.
OUTCE membrane; Porin; Signal; Transmembrane.
OUTCE membrane; Porin; A0312 MW; 9B583F2C11344E31 CRC64;
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LOW A.S., MacKenzie F.M., Gould I.M., Booth I.R.;

"Parallel evolution of multi-resistant bacteria in a patient recurrent septicaemia: unique data that support the presence separate protected environments.";

separate protected environments.";

submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

-I- SUBBUNIT: HOMOTRIMER (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1029.5; DB 2; Pred. No. 1.1e-67;
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Best Local Similarity 57.0
Matches 208; Conservative
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Q9K3E6;
01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000504; -.
InterPro; IPR001702; -.
InterPro; IPR001702; -.
Pfam; PF00267; Gram-ve_porins; 1.
PRINTS; PR00182; ECOLNEIPORIN.
PROSITE; PS00576; GRAM_NEG_PORIN; 1.
PROSITE; PS00030; RNP_1; UNKNOWN_1.
Outer membrane; Porin; Signal; Transmembrane.
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; Y15844; CAB96613.1; -.
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                                                                                                        E-----GIGDVDLVNYFEVGATYYFNKNMSTYVDYIINQIDSDN----KLGVGSDDTVAVG
                                                                                                                                                                                                  AANYGETRNATPI----TNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDV
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LVYQF
                                                                                   SNGYGASYGDQDIVKYVDVGATYYFNKNMSTYVDYKINLLDKNDFTRDAGINTDDIVALG
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378 AA;
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OUTER MEMBRANE PROTEIN C.
, 254524EB9EC3849C CRC64;
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Best Local Similarity
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01-MAY-2000
01-MAY-2000
01-MAR-2001
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InterPro; IPR001702; ...
Pfam; PF00267; Gram-ve_porins; 1.
PRINTS; PR000276; ECOLUBIPORIN.
PROSITE; PS000576; GRAM_NEG_PORIN; 1.
Outer membrane; Porin; Signal; Transı SEQUENCE 366 AA; 40499 MW; 6A4EA
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                                                                                                                                         Q9RAW3
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"Altered outer membrane
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Escherichia
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                                                                                                                                                                                                                                                                                ---DVDLVNYFEVGATYYENKNMSTYVDYIINQIDSDNKL----GVGSDDTVAVGIVYQF
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                                                                                                                                                                                                                                                          NYDDEDILKYVDVGATYYFNKNMSTYVDYKINLLD-DNQFTRDAGINTDNIVALGLFYQF
                                                                                                                                                                                                                                                                                                                                                   QYTQTYNATRV-----GSLGWANKAQNFEAVAQYQFDFGLRPSLAYLQSKGKNLGVINGR
                                                                                                                                                                                                                                                                                                                                                                              NYGETRNATPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGIG---
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; Pred. No. 1.3e-67;
43; Mismatches 71;
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6A4EAD1652565C00 CRC64;
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Matches 196
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"phylogenetic analysis of Calymmatobacterium gububatted (JUN-1997) to the EMBL/GenBank/DDBJ-1-SUBUNIT: HOMOTRIMER (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PR
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prINTS; pR00182; ECOLNEIPORIN: 1.
prOSITE; pS00576; GRAM_NEG_PORIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF009229; AAD21517.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klebsiella pneumoniae (subsp. o:
Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outer membrane; Porin; Signal; Transmembrane NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carter J.S., Bowden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-I436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klebsiella
                                                                                                 01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
PHOSPHATE PORIN (FRAGMENT).
 MEDLINE-20023050; Pocarter J.S., Bowden
                   SEQUENCE FROM N.A. STRAIN-NCTC5046;
                                                                     Bactería;
                                                                              Klebsiella pneumoniae
                                                                                         PHOE
                                                                                                PHOSPHATE PORIN
                                                                                                                              Q9RAW2;
01-MAY-2000
                                                                                                                                                  Q9RAW2
                                                NCBI_TaxID=39831;
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                                                           lebsiella.
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                                                                                                                                                                                                                                                                                                                  WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG
                                                                                                                                                                                                                                                   TPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVDLVNYFEV
                                                                                                                                                                                                                                                                                        YEYEG--FGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAANYGETRNA
                                                                                                                                                                                                                                                                                                                                                                                                 GLTYYFNKNMNAFVDYKINQLKSDNKLGINDDD
                                                                                                                                                                                                             GATYYFNKNMSTYVDYIINQIDSDNKLGVGSDD
                                                                                                                                                                                                                                                                             YDFGGSDFAVSAAYTSSDRTNDQNLLARGQGSKAEAWATGLKYDANNIYLATMYSETRKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001702; -.
                                                                   Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333
333
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PubMed=10555350;
en F.J., Bastian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333
36839 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F.J., Bastian
                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.5%;
                                                                     subsp. rh
ria; gamma
                                                                                                            Last sequence up
                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1022.5; DB pred. No. 3.2e-67;
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ma subdivision; Enterobacteriaceae;
                                                                     rhinoscleromatis
mma subdivision; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68AF347207770ABA CRC64;
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  Η.,
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  Myers
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                                                                       Enterobacteriaceae;
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  Sriprakash
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Best Local S
Matches 196
                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
OUTER MEMBRANE PROTEIN FX PRECURSOR.
OMPEX.
                                                                                                                                                                                                                                                                                                                                                                                                    Q9K3E7
Q9K3E7;
01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00267; Gram-ve_porins; 1.
PRINTS; PR00182; ECCLNEIPORIN.
PROSITE; PS00576; GRAM_NEG_PORIN;
Outer membrane; Porin; Signal; Tr
                                         PRINTS; F
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Phylogenetic
                                                          Submitted (DEC-1997) to the EMB
EMBL; Y15843; CAB96614.1; -.
Interpro; IPR001702; -.
Pfam; PF00267; Gram-ve_porins;
PRINTS; PR00182; ECCLNEIPORIN.
                                                                                                                                                                                                                                                                                                                      Salmonella enterica subsp. Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
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                                                                                                                                                                                                               STRAIN-SF1111;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  Salmonella
                                                                                                                                                                     SOOT
                                                                                                                                                                                             Zimmermann H., Wassenaar T.M., Laubenheimer-Preusse H.,
                                                                                                                                                                                                                                                                            NCBI_TaxID=70803;
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; AF009230; AAD21518.1;
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| ||||||||: :||| |||: ||||||: ||
GLTYYFNKNMNAFVDYKINQLKSDNKLGINDDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WESEFSGNKTESDSSQ----KTRLAFAGVKLKNYGSFDYGRNLGALYDVEAWTDMFPEFGG
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96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001702;
                                             PS00576;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333
; 36839
                                           GRAM_NEG_PORIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.5%;
58.9%;
    22
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                                                                                                                                                                                                                                                                                                                      , enterica serovar Minnesota gamma subdivision; Enteroba
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                                                                                                                                                    EMBL/GenBank/DDBJ
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Pred. No. 3.2
        POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363
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                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae;
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 Query Match 56.9
Best Local Similarity 58.9
Matches 196; Conservative
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Best Local
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Q9RR59;
O1-MAY-2000 (TrEMBLrel. 13, C
O1-MAY-2000 (TrEMBLrel. 13, L
O1-MAR-2001 (TrEMBLrel. 16, L
                                                              NON_TER
SEQUENCE
                                                                                            PRINTS; PRO0182; ECOLNEIPORIN.
PROSITE; PS00576; GRAM_NEG_PORIN; 1.
Outer membrane; Porin; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
SEQUENCE
                                                                                                                                                                                                 "Phylogenetic evidence for reclassification of Calymmatobacterium granulomatis as Klebsiella granulomatis comb. nov."; Int. J. Syst. Bacteriol. 49:1695-1700(1999).
-1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
                                                                                                                                                              (BY SIMILARITY).
EMBL; AF009231; AAD21519.1;
HSSP; P02932; 1PHO.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-20023050; PubMed-10555350;
                                                                                                                                       InterPro; IPR001702; -.
Pfam; PF00267; Gram-ve_porins; 1.
                                                                                                                                                                                                                                                               Carter J.S., Bowden Kemp D.J.;
                                                                                                                                                                                                                                                                                                                                         Calymmatobacterium.
                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                  Calymmatobacterium granulomatis
                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHATE PORIN (FRAGMENT).
                                                                                     NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVGATYYFNKNMSTYVDYIINQIDSDNKLG--VGSDDTVAVGIVYQF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SISYEYEGFGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAANYGETRN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVYYDALGYTDMLPEFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAGATYYFNKNMNVWVDYRFNLLDENDYSSSYVGTDVQAAVGITYQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATPITHKFTHTSGFAHKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGI-GDVDLVNYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DT---AYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNERDTARRS-NGDGVGG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cal Similarity
199; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TMAYEFDGFGVTAAYSNSKRTNDQQDRD-GNGDRAESWAVGAKYDANNVYLAAVYAETRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEYRTKADRAEG-EQQNSNLVRLAFAGLKYAEVGSIDYGRNYGIVYDVESYTDMAPYFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEIYNKDGNKLDLYGKAVGRHVWTT-TGDSK---NADQTYAQIGFKGETQINTDLTGFGQ 78
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333
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363 /
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                                                              ₹
                                                              333
36786 MW;
                                                                                                                                                                                                                                                                           F.J., Bastian I., Myers G.M., Sriprakash K.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40090 MW;
              56.5%;
58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.5%;
                                                                                                                                                                                                                                                                                                                                                     gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.
  41;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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              Score 1021.5;
Pred. No. 3.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OUTER MEMBRANE PROTEIN FX F5058DEDEAS16859 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                              7CEA2F68B998BB0A CRC64;
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Mismatches
            .8e-67
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                         DB 2;
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  79;
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  Indels
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 17;
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                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 196; Conser
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Q9S613;
01-MAY-2000 (TrEMBLTel. 13, C:
01-MAY-2000 (TrEMBLTel. 13, L:
01-MAR-2001 (TrEMBLTel. 16, L:
OUTER MEMBRANE PHOSPHATE PORI)
                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Phylogenetic evidence for reclassification of granulomatis as Klebsiella granulomatis comb. Int. J. Syst. Bacteriol. 0:0-0(1999).
-i- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PR
                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00267; Gram-ve_porins; 1.
PRINTS; PR00182; ECOLMEIPORIN.
PROSITE; PS00576; GRAM_MEG_PORIN; 1.
Outer membrane; Porin; Signal; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF064793; AAD11630.1;
HSSP; P02932; 1PHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-NCTC9633T;
Carter J.S., Bowden F.J., Bastian I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kemp D.J.;
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                        WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG 120
                                                                                                            AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ
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WESEFCGNKTESDSSQ---KTRLAFAGVKLKNYGSFDYGRNLGALYDVEAWTDMFPEFGG
                                                                                           AEVYNKNANKLDVYGKIKAMHYFSDYDSK-----DGDQTYVRFGIKGETQINDDLTGYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDFGGSDFAVSAAYTSSDRTNDQNLLARGQGSKAEAWATGLKYDANNIYLATMYSETRKM
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333
333 AA;
                                                                                                                                                                                       Conservative
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REMBLrel. 13, Last sequence update)
REMBLrel. 16, Last annotation update)
PHOSPHATE PORIN PRECURSOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                           333
36855 MW;
                                                                                                                                                                                                          56.4%;
58.9%;
                                                                                                                                                                                    41;
                                                                                                                                                                                                          Score 1019.5; DB 2; Pred. No. 5.3e-67;
                                                                                                                                                                                                                                                                                                           68AF32C5077705EA CRC64;
                                                                                                                                                                                       Mismatches
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o. nov.";
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                                                                                                                                                                                       Gaps
126
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Best Local Similarity
Matches 198; Conserv
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SEQUENCE
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01-mAR-2001 (TrEMBLrel. 16, Created)
01-mAR-2001 (TrEMBLrel. 16, Last sequence update)
01-mAR-2001 (TrEMBLrel. 16, Last annotation updat
01-mAR-2001 (TrEMBLrel. 16, Last annotation updat
                                                                                                                                                                                                                                                                                                                            "OmpF porin is expressed in Submitted (APR-2000) to the EMBL; AF251685; AAG09474.1;
                                                                                                                                                                                                                                                                                                                                                          STRAIN-9, 12, (VI):D;
Mata-Gonzalez M.T., P
Ortiz-Navarrete V.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhi.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                    Signal.
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella.
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                                                                          DT---AYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNERDTARRS-NGDGVGG
:| ||:|:: | ||:||:||||||:|: : | ||||||
ETWGGAYTDNYMTSRAGGLLTYRNSDFFGLVDGLSFGIQYQGKNQDNHSINSQNGDGVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATYYFNKNMSTYVDYIINQIDSDNKLGVGSDD 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVDLVNYFEV
                                     WEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGG
                                                                                                                                                                                                         ABIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQ
QAGATYYFNKNMNVWVDYRFNLLDENDYSSSYVGTDDQAAVGIV
         EVGATYYFNKNMSTYVDYIINQIDSDNKLG--VGSDDTVAVGIV 337
                                                                                                                                                         WEYRTKADRAEG-EQQNSNLVRLAFAGLKYAEVGSIDYGRNYGIVYDVESYTDMAPYFSG
                                                                                                                                                                                                AEIYNKDGNKLDLYGKAVGRHVWTT-TGDSK---NADQTYAQIGFKGETQINTDLTGFGQ
                                                                                                                                                                                                                                                                                       360
360 AA;
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39665
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                                                                                                                                                                                                                                               56.2%;
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EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                               Score 1017.5; DB 2; Pred. No. 8.3e-67;
                                                                                                                                                                                                                                                                                                            POTENTIAL
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                                                                                                                                                                                                                                                                                         B48A516859F65771 CRC64;
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                                                                                                                                                                                                                                        Mismatches
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Best Local Similarity
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O87753;
O1-NOV-1998 (TrEMBLrel. 08, C
O1-NOV-1998 (TrEMBLrel. 08, I
O1-MAR-2001 (TrEMBLrel. 16, I
OMPK35 PORIN PRECURSOR.
                                                             Q9EXH8 PRELIMINARY;
Q9EXH8;
Q1-MAR-2001 (TIEMBLIEL 16,
01-MAR-2001 (TIEMBLIEL 16,
01-MAR-2001 (TIEMBLIEL 16,
                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                    Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                         Thesis (1998), Universitat de les EMBL; AJ011501; CAA09665.1; -. HSSP; P02931; 1GFN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klebsiella pneumoniae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klebsiella
                      Klebsiella pneumoniae.
Bacteria; Proteobacteria;
Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00182; ECOLNEIPORIN
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001702; -.
Pfam; PF00267; Gram-ve_porins;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hernandez-Alles S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-KT755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
              NCBI_TaxID=573;
                                                OMPK35
                                                       OMPK35
SEQUENCE FROM N.A
                                                                                                                                                                                                                                 136
                                                                                                                                   254
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                                                                                                                                                                                                                                                                TP----EEDNHFAGKTQNFEAVVQYQFDFGLRPSIGYVQTKGKDLQSRAGFSGGDADLV
                                                                                                                                                                           TPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGI-----GDVDLV
                                                      PROTEIN PRECURSOR.
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359 /
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359 OI
39510 MW;
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Pred. No. 9.6e
42; Mismatches
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Last sequence update)
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OMPK35 PORIN.
; 12D518340058E5BB
                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subdivision; Enterobacteriaceae;
                                  subdivision;
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Query Match
Best Local Sim
Matches 159;
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Best Local Similarity
Matches 170; Conserv
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Q9ZC71;
Q9ZC71;
Q1-MAY-1999 (TEMBLIFEL 10, C
Q1-MAY-1999 (TEMBLIFEL 10, L
Q1-MAR-2001 (TEMBLIFEL 16, L
                                                  Buchrieser C., Rusniok C., Couve E., Frangeul L., Billault A.,

Kunst F., Carniel E., Glaser P.;

"DNA sequence of the 102 kbases unstable region of Yersinia pestis.";

submitted (CCT-198) to the EMBL/GenBank/DDBJ databases.

EMBL; AL031866; CAA21336.1; -.

EMBL; AL031867; CAA21336.1; -.

Interpro; IPR001702; -.

Interpro; IPR001702; -.

Pfam; PP00267; Gram-ve_porins; 1.

PRINTS; PR00182; ECCLNEIPORIN.

SEQUENCE 315 AA; 34304 MW; D32FB91828EDA17A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
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Crowley B., Benedi V.J., Domenech-Sanchez A.;
"Expression of altered OmpK35 porin and SHV-2 beta-lactamase in Klebsiella pneumoniae results in cephalosporins and carbapenems resistance.";
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                    Yersinia pestis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                           SIMILAR TO OMPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                              NCBI_TaxID=632;
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          Local Similarity
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315 AA;
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          42.68;
                                                                                                                                                                                                                    gamma subdivision; Enterobacteriaceae;
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 33;
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Pred. No. 4.3e-52;
Pred. No. 4.3e-52;
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          Score 770; DB 2;
Pred. No. 8.4e-49;
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; F45748383475D8CA CRC64;
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 Mismatches
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                     DB 2; Length 315;
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Best Local Similarity
Matches 82; Conserv
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Achouak W., de Mot R., Heulin T.;
FEMS Microbiol. Ecol. 0:0-0(0).
EMBL; U17430; AAA56871.1; -.
HSSP; P09878; 1IIV.
InterPro; IPRO01702; -.
Pfam; PF00267; Gram-ve_porins; 1.
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Q52641;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2001
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SEQUENCE
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Bacteria; Proteobacteria; gamma
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TYGADNFMFQRANGVAT
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                                                                                                     EYQASLNTGESEDA---NNFTRVGFAGLKFGQWGSLDYGRNYGVMYDVAAWTDVLPEFGGD
                                                                                                                             EYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVYDALGYTDMLPEFGGD
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130 AA;
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14510 MW;
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Search completed: Job time: 607 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Minimum DB seq
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Listing first 45 summaries
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length: 2000000000
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1: /SIDS8/gcgdata
2: /SIDS8/gcgdata
  July 3, 2001, 14:50:50 ; Search time 86.32 Seconds (without alignments) 204.374 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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1485
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               /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
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Pred. No. score grea and is No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length DB	BB	ID	Description
_	1036	69.8	606	16	AAR99053	Spider dragline v
N	1036	69.8	606	20	AAY40100	Polymer of an anal
ω	1031	69.4	646	18	AAW27178	Nephila clavipes
4	1015	68.4	651	20	AAY40097	Spider silk prote
5	1015	68.4	718	19	AAW53346	Nephila clavipes s
6	1015	68.4	718	21	AAY59070	N. clavipes spides
7	1001	67.4	718	12	AAR14308	N.clavipes draglin
æ	984	66.3	604	16	AAR99057	Spider dragline v
9	976	65.7	606	16	AAR99055	Spider dragline v
10	976	65.7	606	20	AAY40101	Polymer of an ani
11	976	65.7	606	20	AAY40102	Polymer of an anal

New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells

WPI; 1995-036479/05.

ŕ	4	3	42	41	40	39	38	37	36	ω 5	34	<u>3</u> 3	32	31	30	29	28	27	26	25	24	23	22	21	20	19		17		15	14	13	12
# / 6 . 5	ı	488	488	488	503.5	507	507	507	507	507	520	520	520	520	520	520	520	520	520	524	524	554	554	554	554	561	561	591.5	•		610.5	7	677.5
32.I	32.2	•		•		34.1			34.1			35.0	٠		٠			٠	٠	•	35.3	•			•			•		-		45.4	45.6
TOO	1018	1332	1332	1332	980	1101	1059	1059	1059	1023	1178	1178	1177	1177	1177	1177	1177	1177	1177	714	714	595	595	595	531	235	235	261	738	641	641	831	615
,	3 6	22	22	17	16	21	18	14	9	19	19	14	22	22	21	18	17	11	9	20	16	21	19	12	20	19	17	19	19	21	20	16	20
AARSSIO	AAW01496	AAB63999	AAB72729	AAR95109	AAR81318	AAY78283	AAW26348	AAR41013	AAP82962	AAW53524	AAW53518	AAR41007	AAB63995	AAB72725	AAY78277	AAW26342	AAR95105	AAR05307	AAP80940	AAY40103	AAR99059	AAY59071	AAW53347	AAR14309	AAY40098	AAW79126	AAW05704	AAW79137	AAW56163	AAY95856	AAY28843	AAR80168	AAY40099
בומוסוופנינוו נפדד מ	Silk-like protein	SLP-C protein sequ	Repetitive protein	Silk like protein	Adhesion protein.	SELP4 amino acid s	SLP4 synthetic pro	SLP4 multimeric pr	SEPL4 protein comp	Amino acid sequenc	Amino acid sequenc	Silk-like protein	SLPIII protein seq		I ami			SLP III (Silk-fibr	SlPIII protein com	Polymer of an anal		N. clavipes spider	Nephila clavipes s	pes d	Spider silk protei		Glycine-rich repea	A Gly	New DNA sequence i	Epstein Barr virus	n Barr	Misp	silk

ALIGNMENTS

RESULT AAR99053

Spider; dragline protein; variant; monomer; polymer; fibre forming region; Spidroin 1; Nephila clavipes; DP1; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope; surgical suture; implant; reinforcement; film; coating. Synthetic. Spider dragline variant, DP-1A.9 polymer. 17-JAN-1997 (first entry) AAR99053; AAR99053 standard; Protein; 606 Fahnestock SR; (DUPO) DU PONT DE NEMOURS & CO E 15-JUN-1993; 15-JUN-1994; 22-DEC-1994. WO9429450-A2. 93US-0077600. 94WO-US06689. ₿ Н

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RESULT
AAY40100
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AC AAY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC The polypeptide monomer is a variant based on a consensus sequence cc derived from the fibre forming regions of spider dragline protein, CC esp. the natural protein 1 (Spideroin 1) from Nephila clavipes.

CC DNA sequence encoding the monomer may be used in the recombinant cc production of the variant protein in a recombinant host, e.g. E. coli cor Bacillus subtilis. Synthetic analogues of DP1 were designed to minic cc or trepeating consensus sequence of the natural protein and the pattern cc of variation among individual repeats. DP-1A analogues are composed co fa tandemly repeated 101 amino acid monomer which comprises four crepeats which differ from the consensus sequence given in AAM06201, CC according to the pattern (1)-(5) given below. This 101 amino acid monomer is repeated 1-16 times in a series of analogue proteins. The cc individual repeats differ from the consensus according to the pattern: (2) when the entire poly-alanine sequence is deleted, co also is the surrounding sequence varies in length from 0-7 cc (3) aside from the poly-alanine sequence, deletions usually cc (4) deletion of GVG is generally accompanied by deletion of GRG coleted is generally preceded by a repeat containing six alanine sequence is coleted is generally preceded by a repeat containing six alanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
 AAY40100;
                                       AAY40100 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                      140
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                                                                         N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents a synthetic spider dragline variant polymer, A.9. The sequence of the DP-1A.9 monomer is given in AAR99052.
                                                                                                                                                                 YGGLGSQG 279
                                                                                                                                                                                                                                         GYGGLGSQGTSGRGGLGGQGAGAAAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSMASGRGGLGGQGAGAAAA-----
                                                                                                                              ygglgsqg
                                                                                                                                                                                                   gygglgsqg-agrgglggqgagaaaaaaaggagqgglgsqgagqagaaaaaaggagqgg
                                                                                                                                                                                                                                                                         gqgagaaaaaaggagqggygglgsqgagqggygglgsqagagaaaaaggagqg
                                                                                                                                                                                                                                                                                              ----AAAAAAGGAGQGGYGGLGSQGT--SGRGGLGGQGA---GAAAAAAAAAAAGGAGQG
                                                                                                                                                                                                                                                                                                                                                  ggqgagaaaaaaaggagqggygglgsqg-agrgglggqgagaaaaaaaggagqgglgsqga
                                                                                                                                                                                                                                                                                                                                                                                      -GAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAA------
                                                                                                                                                                                                                                                                                                                                                                                                                      aaaaaggagqgglgsqgagqagaaaaaaggagqggygglgsqgagqggygglgsqgagr 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qgagqggygglgsqgagrggqgagaaaaaaggagqggygglgsqg-agrgglggqgagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGT--SGRGGLGGQGA---GAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gsqgagrgglggqgagaaaaaaggagqgglgsqgagqagaaaaaaggagqggygglgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 85-87; 168pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                392
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                                     protein; 606 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
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Pred. No. 3.3e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----AAAAAAGGAGQGGYGGLGS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 102;
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                                                                                                                                                                                                                                       -AAAAAAGGAGQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 606;
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 239
                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a polymer of an analogue of the spider silk protein spidroine major 1. The protein improves the moisturizing/ softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Peptide
                                                                                                                                                                                                                                                                                                                                                              hormones, moisturizers or agents for treating disorders of the \operatorname{skin} and \operatorname{hair}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscrehormone; moisturizer; skin disorder; skin disorder.
                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                           11 GSMASGRGGLGGQGAGAAAA-----
gqgagaaaaaggagqggygglgsqgagqggygglgsqgagrggqgagaaaaaggagqg
                                                                                                                                                           1999-510729/43
                          ----AAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGGQGA---GAAAAAAAAAAAGGAGQG
                                                   ggqgagaaaaaaggagqggygglgsqg-agrgglggqgagaaaaaaaggagqgglgsqga
                                                                 gsqgagrgglggqgagaaaaaaaggagqgglgsqgagqagaaaaaaggagqggygglgs
                                                                                                                                   AA-----
                                                                                                                                                                                     QGT--SGRGGLGGQGA---GAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Fig
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                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                       606
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                                                                                                                                                                                                                                                                                  69.8%;
64.9%;
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                                                                                                                     Arraudeau
                                                                                                                                                                                                                                                                   Score 1036; DB 20;
Pred. No. 3.3e-73;
4; Mismatches 23;
                                                                                                                                                                                                                                           ------AAAAAAGGAGQGGYGGLGS 49
                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sunscreen;
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RESULT
AAW271178
ID AAW2
XX AAW2
XX AAW2
XX AAW2
XX Neph
XX High
KW High
KW Abso
KW Flav
OS Neph
XX Neph
XX WO97
PN WO97
XX 22-A
XX (BAS
PA (BAS
PA (ELI
PT CON1
PT CO
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                                                                                                                                                                                                                                                              CC A process has been developed for the production of a DNA fragment CC encoding silk protein. The process involves: (a) selecting target DNA, CC from a silk-producing spider, that contains many repetitive and non-cC repetitive regions; (b) selecting a single-stranded DNA primer of at CC least 10 nucleotides with a sequence that is complementary to a region CC of the target; (c) repetitively combining the primer with melted target CC DNA, incubating the mixture with nucleotides and a DNA polymerase with CC proofreading activity to produce a DNA fragment which is complementary CC to the target and is at least 2 kb long. The present sequence encodes the spider silk protein from Nephila clavipes. The DNA fragment can be used to make fibres, films, woven articles, e.g. for use in parachites, CC used to make fibres, films, woven articles, e.g. for use in parachites, cails, body armour, and absorbers (e.g. of heavy metals, biological CC weapons, DNA, chemicals, flavours and fragrances). The high molecular CC weight (90-250 kD) of spider silk proteins can be produced on a CC commercial scale (at over 2 g/1 cell mass). It has better tensile compared the content of both repetitive regions ensures isolation of stable clones.
                                                          Query Match
Best Local Similarity 55.9
Matches 244; Conservative
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New opt. multimerised DNA sequences encoding spider silk protein contg. both repetitive and non-repetitive sequences, useful for making high strength films, fibres, woven articles etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Basel RM, Elion GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAR-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW27178 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 1; 57pp; English.
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The present sequence represents the natural spider silk protein spidroine major 1. The protein improves the moisturizing/softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin
                                                                                                                                                                                          Claim 3; Fig 1; 32pp; French.
                                                                                                                                                                                                                                             Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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Best Local Sim:
Matches 238;
                                                                                                                                                                    15-APR-1991;
20-APR-1990;
04-OCT-1994;
19-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins, hormones, moisturizers or agents for treating disorders of the skin and hair.
WPI; 1998-270437/24.
N-PSDB; AAV23249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spider; Nephila clavipes; cocoon; tensile strength;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nephila clavipes spider silk protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW53346 standard;
                                                                          Hinman
                                                                                                                                                                                                                                                                                                                                                                                                                                       Nephila clavipes.
                                                                                                                          (UYWY-) UNIV WYOMING
                                                                                                                                                                                                                                                                                              19-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 ggagqgyygglgnqgagrggqgaaaaaggagqggygglgsqg 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gegagaaaaaaggagqggygglggqgagqggggggggggagaaaaggag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggqgagaaaaaaaggagqgglggqgagqgagasaaaaggagqggygglgsqg----agrg
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                                                                          MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                        Lewis RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                    91US-0684819.
90US-0511792.
94US-0317844.
95US-0425069.
                                                                                                                                                                                                                                                                                            95US-0425069
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59.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      silk protein; tandem
elasticity.
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Pred. No. 1.5e-71;
8; Mismatches 14;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
15-APR-1991;
20-APR-1990;
                                                                          04-OCT-1994;
                                                                                                                                                                      US5989894-A
                                                                                                                                                                                                                                                                      Spider silk protein; dragline silk protein; major ampullate gland; fiber.
                                                                                                                                                                                                                                                                                                                      N. clavipes
                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                        AAY59070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY59070 standard; Protein;
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                                                                                                                        23-NOV-1999
                                                                                                                                                                                                                       Nephila clavipes
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                                                                                                                                                                                                                                                                                                                      spider silk protein 1.
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90US-0511792
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59.2%;
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Pred. No. 1.6e
8; Mismatches
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1.6e-71;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins. The spider silk proteins are characterized by repeating alpha and beta regions and optional variable regions. The DNA sequences are useful in the production of spider silk protein by a combinant DNA techniques. The recombinant spider silk proteins may be used for the production of fibers. The present sequence represents the spider silk protein 1, derived from the major ampullate gland of Nephila clavipes.
                                                                                   N.clavipes dragline
                                                                                                            15-JAN-1992
                                                            protein superfibre;
                                                                                                                                     AAR14308
                                                                                                                                                             AAR14308 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 6A-D; 65pp; English.
              EP452925-A
                                     Nephilia clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides isolated cDNA molecules coding for spider silk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated DNA, vector and the production of spider
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                                                                                                                                                                                    7
                                                                                                                                                                                                                       ggagqggygglgnqgagrggqgaaaaaggagqggygglgsqg
                                                                                                                                                                                                                                                                                                                                   GQGAGAAAAAAAAAA - - - - - - AGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAA - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggygglgsqgagrggqgagaaaaaaaggaggrgygglgnqg-agrgglggqgagaaaaaaa
                                                                                                                                                                                                                                                                                                                       qgglggqgagagaaaaaggagqggygglgsqg-agrgglggggagavaaaaaggagq
                                                                                                                                                                                                                                                                                                                                                                      gegagaaaaaaggagqggygglggqgagqggygglgsqg-agrgglggqgagaaaaggag
                                                                                                                                                                                                                                                                                                                                                                                                                     ggqgagaaaaaaaggagqgglggqgagqgagasaaaaggagqggygglgsqg----agrg
                                                                                                                                                                                                                                                                                                                                                                                                                                               GGQGAGAAAAAA-----AAAAGGAGQGGYGGLGSQGTSGRGGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLGSQGTSGRGGLGGQGAGAAAAAAAAA-----AGGAGQGGYGGLGSQGTSGRGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gsqgagrgglggqgagaaaaaaggagqggygglgnqgagrggggaaaaaaggagqggyg 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSMASGRGGLGGQGAGAAAA------AAAAAAAGGAGQGGYG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-061225/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    718 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xu M, Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                            (first
                                                                                                                                                                                                                                               ------AAAAAGGAGQGGYGGLGSQG
                                                                                                                                                                                                                                                                                  Protein;
                                                                                   silk protein-1
                                                                                                            entry)
                                                            major ampullate silk; orb web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.4%;
59.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transformed cell encoding silk protein -
                                                                                                                                                                                                                                   8;
                                                                                                                                                             718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1015;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                             ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
..6e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                        485
                                                                                                                                                                                                                                               279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for and
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AAR99057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The spider silk protein contains a basic 34 amino acid repeat. The repeat itself contains 3 regions. The first comprises 0-9 amino acids with a sequence ARG(GSX)2. This region is not highly conserved. The second region has a sequence GAG(A)x which is highly conserved and is 8-10 amino acids long. The third segment is (GGX)2 and is 15 amino acids long and is very highly conserved. In most cases X is A,O, Y or L. Removal of the poly-(Ala) segments results in a silk having lower elasticity.
                                                                              AAR99057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 23; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding spider silk protein-1 and 2 and variants - isolation Nephila clavipes, for productor of spider silk protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ14183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis RV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibres having desired characteristics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYWY-) UNIV OF
                                                                                                                                          444 ggagqggygglgnqgagrggqgaaaaaggagqggygglgsqg
                                                                                                                                                                                                                                                                                                   267
                                                                                                                                                                                                                                                                                                                                                      211
                                                                                                                                                                                            385 ggygglgsqgagrggqgagaaaaaaggagqrgygglgnqg-agrgglggqgagaaaaaa
                                                                                                                                                                                                                                              326 qgglggqgagqgagaaaaaaggagqggygglgsqg-agrgglggqgagavaaaaaggagq
                                                                                                                                                                                                                                                                                                                            136 GQGAGAAAAAAAA-----AGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAA----
                                                                                                                                                                                                                                                                                                                                                                                                     97 GGQGAGAAAAAA------AAAAGGAGQGGYGGLGSQGTSGRGGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                  46 GLGSQGTSGRGGLGGQGAGAAAAAAAAA-----AGGAGQGGYGGLGSQGTSGRGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 gsqgagrgglggggagaaaaaaaggaggggggglgnqgagrggggaaaaaaggagqggyg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 GSMASGRGGLGGQGAGAAAA------
                                                                                                       8
                                                                                                                                                                                                                                                                                               1991-312199/43
                                                                                                                                                                                                                                                             ggqgagaaaaaaaggagqgglggqgagqgagasaaaaggagqggygglgsqg----agrg
                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            718 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hinman M;
                                                                                                                                                                                                          -----AAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAA---
                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.4%;
58.7%;
                                                                                                                                                        ------AAAAAGGAGQGGYGGLGSQG 279
                                                                              604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1001; DB 12; Pred. No. 1.9e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AAAAAAGGAGQGGYG
                                                                                                                                             485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                135
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13;

Spider dragline variant, DP-1B.16 polymer.

17-JAN-1997 AAR99057;

(first entry)

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derived from the fibre forming regions of spider dragiline protein,
cesp. the natural protein 1 (Spidroin 1) from Nephila clavipes. The
CDNA sequence encoding the monomer may be used in the recombinant
CC DNA sequence encoding the monomer may be used in the recombinant
CC or Bacillus subtilis. Synthetic analogues of DP1 were designed to mimic
CC or Bacillus subtilis. Synthetic analogues of DP1 were designed to mimic
CC the repeating consensus sequence of the natural protein and the pattern
CC the natural sequence which is not shared by DP-1A, namely that a repeat
CC the natural sequence which is not shared by DP-1A, namely that a repeat
CC the natural sequence which is not shared by DP-1A, namely that a repeat
CC the sequence of DP-1B matches the natural sequence more closely over
CC a more extended segment than does DP-1A.
CC The sequence of DP-1B matches the natural sequence more closely over
CC a more extended segment than does DP-1A.
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the sequence (2) when the entire poly-alanine sequence is deleted,
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the sequence (2) when the entire poly-alanine sequence is deleted,
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the sequence varies in length from 0-7
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the poly-alanine sequence varies in sequence is deleted,
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the poly-alanine sequence varies in length from 0-7
CC (1) the
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spider; dragline protein; variant; monomer; polymer; fibre forming region; Spidroin 1; Nephila clavipes; DP1; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope; surgical suture; implant; reinforcement; film; coating.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a synthetic spider dragline variant polymer DP-1B.16. The sequence of the DP-1B.16 monomer is given in AAR99056 The polypeptide monomer is a variant based on a consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 106-108; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-036479/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fahnestock SR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the same sequence; and (5) a repeat in which the entire poly-alanine sequence is deleted is generally preceded by a repeat containing six alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                  1
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                                                                                                                                                                                              gsqgagrgglggqgagaaaaaaaggagqgglgsqgagagaaaaaaggagqggygglgs
                                                                                                                                                                                                                                                                                                  GSMASGRGGLGGQGAGAAAA--------AAAAAAGGAGQGGYGGLGS 49
--- bb
                                                                                                    QGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGT-----SGRGGLG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DU PONT DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is the surrounding sequence encompassing AGRGGIGGGGAGANGG;
(3) aside from the poly-alanine sequence, deletions usually se integral multiples of three consecutive residues;
(4) deletion of GYG is generally accompanied by deletion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9305-0077600.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         66.3%;
9166x6ebs6166x66be6bs6166x6b6b6b6b6beepee.
                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 984; DB 16; Pred. No. 3.4e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 604;
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                      136;
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                        72
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밁 οy В Ş

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RESULT
AAR89055
ID AAR8
XX AAR89055
AC AAR8
XX Spid
XX
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This sequence represents a synthetic spider dragline variant polymer, pp-1B.9. The sequence of the DP-1B.9 monomer is given in AAR99054. The polypeptide monomer is a variant based on a consensus sequence derived from the fibre forming regions of spider dragline protein, esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. The DNA sequence encoding the monomer may be used in the recombinant production of the variant protein in a recombinant host, e.g. E. coli or Bacillus subtilis. Synthetic analogues of DP1 were designed to mimic the repeating consensus sequence of the natural protein and the pattern of variation among individual repeats. This monomer exhibits all of the regularities of (1)-(5) below. In addition, it exhibits a regularity of the natural sequence which is not shared by DP-1A, namely that a repeat in which both GYG and GRG are deleted is generally preceded by a repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spider; dragline protein; variant; monomer; polymer; fibre forming region; Spidroin 1; Nephila clavipes; DP1; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope; surgical suture; implant; reinforcement; film; coating.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 88-90; 168pp; English.
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Best Local Similarity
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Peptide
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(1) the poly-alanine sequence varies in length from 0-7 residues; (2) when the entire poly-alanine sequence is deleted, so also is the surrounding sequence encompassing ARRGGLGGGARANGG; (3) aside from the poly-alanine sequence, deletions usually encompass integral multiples of three consecutive residues; (4) deletion of GYG is generally accompanied by deletion of GRG in the same sequence; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
                                                                                                                                                                                                                             Spider silk protein; spidroine major 1; dermatological compositions; hair care;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY40101 standard;
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                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                Polymer of an analogue of spider silk protein spidroine major 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY40101;
                                                                                                              Nephila clavipes
                                                                                                                                                                                                  hormone; moisturizer; skin disorder; skin disorder
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is generally preceded by a repeat containing six alanine
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pred. No. 1.4e-68;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a polymer of an analogue of the spider silk protein spidroine major 1. The protein improves the moisturizing/softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make up or sunscreens. As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins, hormones, moisturizers or agents for treating disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Fig 5B; 32pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  skin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-1998; 98FR-0001614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OREA ) L'OREAL SA
                                                                                                                                                                                                                                                                                                                          125
                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                    349 qgagqgagaaaaaaggagqggygglgsqg 377
                                                                                                                                                                                       224 AAAGGAGQGGYGGLGSQGT------SGRGGLGGQGAGAAAA-----
                                                                                                                                                                                                               237 aggagqgglgsqgagqagaaaaaggaggggggglgsqg----agrggqgag----aaa
                                                                                                                                                                                                                                                                                                                                                    86
                                                                                                                                                                                                                                                                                                                                                                               73
                                                                                                                                                                                                                                                                                                                                                                                                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                13 gsqgagrgglggqgagaaaaaaggagqgglgsqgagqagaaaaaggagqggygglgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                             QGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGT------SGRGGLG
                                                                                                                                                           aaaggagqggygglgsqgagqggygglgsqgagrgglgggggagaaaaaaggagqgglgs
                                                                                                                                                                                                                                                                    qgag----aaaaaaggagqggygglgsqgagqggygglgsqgagrgglggqgagaaaaa
                                                                                                                                                                                                                                                                                                                        gqgagaaaaaaaggagqgglgsqgagqagaaaaaaggagqggygglgsqg----agrgg
                                                                                                                                                                                                                                                                                                                                                    GQGAGAAAA-----AAAAAAGGAGQGGYGGLGSQGTSGRGGLGG
                                                                                                                                                                                                                                                                                                                                                                            qg----agrggggag----aaaaaaggaggggggglgsqgagggggggglgsqgagrgglg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         606 AA
                                                                                                                                   -- AAAAAAGGAGQGGYGGLGSQG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garson JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98FR-0001614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 976; DB 20;
Pred. No. 1.4e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                 182
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AAY40102

AAY40102 standard;

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscreen; hormone; moisturizer; skin disorder; skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cosmetic or
for hair or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-510729/43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 6B; 32pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Philippe M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (OREA ) L'OREAL SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nephila
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                  179
  224
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                                                                                                                                       123
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                                                                                                                                                                                                                                            gsqgagrgglggqgagaaaaaaaggagqgglgsqgagqagaaaaaaggagqggygglgs 70
                                                                                                                                                                                                                                                                  QGAGAAAAAAAAAAGGAGQGGYGGLGSQGT-----SGRGGLGGQGAGAAAA--
                                                                                                                                                                  GQGAGAAAA-----
  AAAGGAGQGGYGGLGSQGT------SGRGGLGGQGAGAAAA---
                                                                              qgag----aaaaaaggagqggygglgsqgaqqgygglgsqgagrgglggqgagaaaaaa 234
                                                                                                                                      gqgagaaaaaaaggagqgglgsqgagqgagaaaaaaggagqggygglgsqg----agrgg
                                                                                                                                                                                          qg----agrggggag----aaaaaaggaggggggglgsqgagqggygglgsqgagrgglg
                                                                                                                                                                                                                     QGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGT-----SGRGGLG
                         aggagqgglgsqgagqaaaaaaaggagqggygglgsqg----agrggqgag----aaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of an
                                                                                                                                                                                                                                                                                                                                                                          606 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dermatological composition skin care, in make-up or su
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garson JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                               analogue of spider silk protein spidroine major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98FR-0001614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98FR-0001614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "monomer unit"
                                                                                                                                                                                                                                                                                                                     65.7%;
59.1%;
                                                      ----AAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAA 223
                                                                                                                                                                                                            Arraudeau JP;
                                                                                                                                                                 -----AAAAAAGGAGQGGYGGLGSQGTSGRGGLGG 136
                                                                                                                                                                                                                                                                                                        4.
                                                                                                                                                                                                                                                                                                     Score 976; DB 20;
Pred. No. 1.4e-68;
4; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on containing spider silk protein, sunscreens
                                                                                                                                                                                                                                                                                                                                  Length 606;
                                                                                                                                                                                                                                                                                                          Indels 144;
                                                                                                                                                                                                                                                                                                          Gaps
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spider silk protein; spidroine minor 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscreen; hormone; moisturizer; skin disorder; skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                      Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spider silk protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY40099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY40099 standard; protein; 615
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                         skin and hair.
                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Fig 3; 32pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-510729/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Philippe M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347
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                           110 AAAGGAGQGGYG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qgagqgagaaaaaaggaggggggglgsqg 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aaaggagggygglgsqgagqgygglgsqgagrgglggqgagaaaaaaggagggggg 346
--GAGAAAAAAAAAGGAGQGGYG----GLGSQGTSGR-------GGLGGQGAGAAAAAAA 109
                                                                                                                gagagagaaaaaagagsggaggygrgagagagaaagagagagsygggggggggagagaaaa
                                                                                                                                                      167;
                                                                                                                                                                  Similarity
                                                                                                                                                                                                                  615 AA;
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spidroine minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                45.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arraudeau JP;
                                                                                                                                                      10; Mismatches
                                                                                                                                                     Score 677.5; DB 20;
pred. No. 1.7e-45;
10; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₿
                           ---GLGSQGT----SGRGGLGGQGAGAAAAAAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                             Length 615;
                                                                                                                                                        83;
                                                                                                                                                       Gaps
                                                       179
                                                                                                         119
       239
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RESULT 1
AAR80168
AD AAR80168
AX AAR8
AX AAR8
AX AAR8
AX AAR8
AX AAR8
AX Spid
KW Spid
XX Neph
AX Spid
XX Sepid
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Query Match
Best Local Similarity
Matches 168; Conserv
                                                                                                                                                                             This sequence represents the product of cDNA clone, pMTSS1, encoding the orb web spider minor ampullate silk protein MiSP1 has been identified and sequenced. Repeat unit peptides of MiSP1 may form part of a larger polypeptide with an amino terminus (see AAR80184-85) and a carboxy terminus (see AAR80186-89). Repeat unit peptides make up spider silk proteins (spidroins) which in turn aggregate to form the silk fibres. Spider silk fibres have high tensile strength and significant elasticity. An isolated cDNA clone of a silk protein encoding sequence is of use to produce the protein at high yields using recombinant DNA technology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 1; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide(s) comprising repeated unit amino acid sequences, cDNAs - derived from minor ampullate spider silk proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colgin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9525165-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spider silk; repeat unit; consensus; minor ampullate silk protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pMISS1 MiSP spider silk protein insert product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR80168;
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                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spidroin; Misp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        form spider silk fibres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lewis RV;
                                                                                                                                   831
  Conservative
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272..285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                      45.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "represented as indeterminate, corresponds
to a highly compressed GC rich region in
AAQ98470 which could not be sequenced"
                         Score 674;
Pred. No. 4
  Mismatches
4; DB 16;
. 4.1e-45;
tches 97;
                                               Length 831;
  Indels
  90;
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lused
  Gaps
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RESULT 1
AAX728443
IID AAX72
XX AAX72
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                                                                                                                                                                                                                                                                                                                                                                                          Epstein Barr Virus Nuclear Antigen 1; plasmid pcMVEBNA; EBNA 1; episome; transfection; origin of replication; EBV orip; receptor; eucaryotic host cell; recombinant cell line; ion channel; gene thera multiple gene expression; transporter protein; transcription factor; adhesion molecule; antisense therapy; gene amplification;
              Claim 2; Fig 2; 86pp; English
                                      New method for expressing genes useful for gene therapy -
                                                                               WPI; 1999-610610/52.
N-PSDB; AAX90924.
                                                                                                                                                                           18-MAR-1998;
06-AUG-1998;
                                                                                                                                                                                                                                              23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                        Epstein-barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Epstein Barr Virus Nuclear Antigen 1 (EBNA 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY28843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY28843 standard; Protein;
                                                                                                                                                (PHAR-) PHARMACOPETA INC
                                                                                                                                                                                                                   12-FEB-1999;
                                                                                                                                                                                                                                                                         W09947647-A1
                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                   cell immortalisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236. ---GLGS-----QGTSGRGGLG-GQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGIRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AAAAGGAGQGGYGGLGSQG------TSGRGGLGGQGAGAAAAAAAAAAAAGGAGQG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 GLGSQGT-----SGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gqggygagaragaaaaagagaggaagysrggragaagagagaaagagagaggyggqggyg
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                                                                                                                        BB,
                                                                                                                        Horlick RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                          98US-0040961
98US-0130114
                                                                                                                                                                                                                   99WO-US03307
                                                                                                                                                                                                                                                                                                                Location/Qualifiers 267
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                                                                                                                        Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 641
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                                                     from
                                                     recombinant eukaryotic cells
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RESULT 15
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Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) obtained from commercially available plasmid pCMYEBNA. EBNA 1 protein is used to stably maintain episomes containing EBV origin of replication (orip) and a gene encoding protein or RNA of interest. Eucaryotic host cells expressing EBNA 1 protein are transfected with the episomes to produce recombinant cell lines expressing multiple genes of interest. This provides a rapid and reliable method of stably expressing multiple genes in transfected cells. The episomes are useful in the transfection of genes encoding receptors, transporter proteins, ion channels, adhesion molecules and transcription factors. The episomes carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy,
Stably transfecting eukaryotic cells with at least one episome
                                                                                                                                                                                                                                                                                                                                                                                     07-NOV-2000 (first entry)
                                                WPI; 2000-515062/46.
                                                                                 Horlick RA,
                                                                                                                                                11-FEB-1999;
                                                                                                                                                                                                             17-AUG-2000
                                                                                                                                                                                                                                                                            Epstein-barr virus
                                                                                                                                                                                                                                                                                                        gene therapy.
                                                                                                                                                                                                                                                                                                                                                       Epstein Barr virus nuclear antigen 1 protein (EBNA1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY95856 standard; Protein; 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                               (PHAR-) PHARMACOPEIA INC
                                                                                                                                                                              11-FEB-2000; 2000WO-US03547.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RGSHHHHHHGSMASGRGGLG-GQGAGAAAAAAAAAAAGGAGQ-GGYGGLGSQGTSGRGGLG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene amplification, cell immortalisation, etc
                                                                                                                                                                                                                                                                                                                         nuclear antigen 1; EBNA1; episome; transfection; selection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aggaggagaggagaggagaggg----rgrggsggrgrggsggrgrggsggrr 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGIR 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGAGAAAAAAAAAGGAGQGGYGGLGSQGTSG----RGGLGGQGAGAAAAAAAAAAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQGGYGGLGSQGTSGRGGLGGQ-GAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGG
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                                  AAA50254.
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                                                                                 Chelsky
                                                                                                                                              99US-0249585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.1%; Score 610.5; DB 20; Length 641; 48.6%; Pred. No. 2.7e-40;
                                                                                 Ö
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   for
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Sequence

641 AA;

factors, such as antibiotics.

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first and second proteins and the selectable marker are expressed, cand the selective pressure specified by the marker is maintained. Under these conditions, only cells containing both episomes live. Preferably, EBNAI is expressed from 1 of the episomes, and the protein of interest from the other episome. Either or both epitopes may further comprise a nucleic acid sequence encoding a protein desired to be expressed in the cell (e.g. a therapeutic protein), a nucleic acid encoding an RNA that is not intended to be translated (e.g. a therapeutic RNA), or a DNA sequence used as a tag for the cells. The method is applicable to cell culture or intact organisms, for gene therapy. It allows the rapid establishment of eukaryotic cells that stably and reliably express a gene of interest, using a novel method of selection, and maintenance of that selection without the need for exogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of DNA encoding the Epstein-Barr virus (EBV) nuclear antigen protein 1 (EBNA1). EBNA1 is utilised in a novel method for obtaining a eukaryotic cell that is stably transfected with at least one episome. This method involves transfecting a eukaryotic cell with: (1) a first episome comprising an EBV origin of replication (orig. see AAA50253), a gene encoding a first protein whose expression results in cell death and a selectable marker for eukaryotic cells; and (2) a second episome comprising an EBV orip and a gene encoding a second protein, where expression of the second protein prohibits the occurrence of cell death resulting from expression of the first protein to produce death resulting from expression of the first protein to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        doubly transfected cells which also express an antigen that promotes retention of the episomes by the cells. The double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production of a desired protein in vitro and for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transfected cells are maintained under conditions in which the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 2; 53pp; English.
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23

Ş 밁 Ş 밁 Š 밁 Ω 밁 δÃ Query Match 41.1%; Score 610.5; DB 21; Length 641; Best Local Similarity 48.6%; Pred. No. 2.7e-40; Matches 189 131 305 2 RGSHHHHHHGSMASGRGGLG-GQGAGAAAAAAAAAAAGGAGQ-GGYGGLGSQGTSGRGGLG 59 GQGGYGGLGSQGTSGRGGLGGQ-GAGAAAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGG 174 QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGIR QGAGAAAAAAAAAAAAGGAGQGYGGLGSQGTSG----RGGLGGQGAGAAAAAAAAAAAGGAG gagggaggaggagggaggggaggggaggaggggagagggaggaggaggaggaggagg 143; Conservative -ggtgagagagagagaggaggaggaggaggaggaggagga 14; Mismatches 104; Indels 33; Gaps 188 244 304 10;

Search completed: July Job time: 436 sec ω 2001, 14:58:06

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                  Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq
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length: 2000000000
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Match
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1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               July 3, 2001, 14:47:50; Search time 48.42 Seconds (without alignments) 121.068 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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1485
      193259 seqs, 20144635 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRGSHHHHHHGSMASGRGGL.....YGGLGSQGTSGIRRPAAKLN
       Length
   BG
US-08-425-069-2
US-09-034-177-3
US-09-034-177-3
US-08-209-747-2
US-08-458-209-2
US-08-458-209-3
US-08-458-209-3
US-08-458-209-4
US-08-475-411A-31
US-08-475-411A-31
US-08-475-411A-31
US-08-475-411A-31
US-08-475-411A-31
US-08-475-411A-31
US-08-475-411A-31
US-08-475-411A-31
US-08-475-411A-36
US-09-060-716-72
US-09-475-411A-36
US-09-060-716-72
US-09-475-411A-36
US-08-475-411A-36
US-08-475-411A-36
US-08-475-411A-36
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US-08-475-411A-36
US-08-475-411A-36
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Description
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11 GSMASGRGGLGGQGAGAAAA--

Query Match
Best Local Similarity 59.3
Matches 238; Conservative

68.48; 59.28;

8

Score 1015; DB 1; Pred. No. 2.8e-75; B; Mismatches 14;

Length 718;

-AAAAAAGGAGQGGYG 45 Indels 142;

Gaps

13;

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UULT 1 equence 2, Application atent No. 5728810 general INFORMATION: APPLICANT: Lewis, Ra APPLICANT: Xu, Ming APPLICANT: Xu, Ming APPLICANT: NUNETION: TITLE OF INVENTION: INUMBER OF SEQUENCES: CORRESPONDENCE ADDRES ADDRESSEE: Birch, STATE: Virginia COUNTRY: U.S.A. ZIP: 22046 COMPUTER READABLE FOR MEDIUM TYPE: Flopp COMPUTER: ELAPPLICATION NUMBER: SOFTWARE: Patentin CURRENT APPLICATION NUMBER: FILING DATE: 19-AP CLASSIFICATION NUMBER: FILING DATE: 19-AP CLASSIFICATION NUMBER: FILING TON NUMBER: FILING TON INF REGISTRATION NUMBER: FILECOMMUNICATION INF TELEPHONE: (703) 2 TELETAX: (703) 2 TELETAX: (703) 2 TELETATION FOR SEQ ID SEQUENCE CHARACTERIST LENGTH: 718 amino TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: prote 08-425-069-2	468.55 468.55 468.68 468.68 688.69
12, Applicati 2, Applicati 2, Applicati 3, 5728810 INFORMATION: INFORMATION: INFORMATION: INFORMATION: OF INVENTION OF INVENTION OF INVENTION OF EQUENCE ADD RESSEE: Birc RESSEE: Glun RESSEE: Virginia RESSEE: Virginia RESSEE: Paten RESSEE: RESSEE: RESSEE RESSEE RESSEE: RESSEE RESSEE: RESSEE RESSEE: RESSEE	
Applicati Applicati Applicati Applicati CATABAIO ORMATION: Lewis, Lumin INVENTION INVENTION INVENTION SEQUENCE 301 No. SEQUENCE 301 No. SEQUENCE 301 No. Falls Chu Virginia U U.S.A. READABLE TYPE: F1 TYPE: F1 TYPE: F1 ICATION NUM ATION NUM ATION NUM ATION NUM ATION NUM ATION NUM CONTROL OFFICATION	333333333333333333333333333333333333333
2 Application 728010 ORMATION: Lewis, Ra INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: SEQUENCES: DENCE ADDRES EE: Birch, 301 No. 57 10 S.A. 301 No. 57 301	u u u u u u o o ∨ a a a a o o o o o o o
T 1 -425-069-2 uence 2, Application US/084250 uent No. 5728810 NERAL INFORMATION: APPLICANT: Lewis, Randolph V. APPLICANT: Hinman, Michael B. TITLE OF INVENTION: ISOLATED I TITLE OF INVENTION: PROTEIN, J TITLE OF INVENTION: CONTAININ NUMBER OF SEQUENCES: 69 CORRESPONDENCE ADDRESS: ADDRESSEE: Birch, Stewart, J STREET: 301 No. 5728810th W. CITY: Falls Church STATE: Virginia , COUNTRY: U.S.A. , ZIP: 22046 COMPUTER READABLE FORM: MEDIUM TYPE: Tloppy disk COMPUTER IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: PATENTIN Release: CURRENT APPLICATION NUMBER: US/08/4: FILING DATE: 19-APR-1995 CLASSIFICATION INFORMATION: APPLICATION NUMBER: US/08/4: FILING DATE: 19-APR-1995 CLASSIFICATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 144 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8050 TELEX: LENGTH: 718 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: protein -425-069-2	7666 7666 7666 7666 7666 7784 784 784 334 4870 649 945
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                                                                                                                                                               EILING DATE: 04-CCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPLY Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                          TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
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APPLICANT: Hinman, Michael B.
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DA
TITLE OF INVENTION: PROTEIN, A
TITLE OF INVENTION: CONTAINING
NUMBER OF SEQUENCES: 62
                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: U$/08/317,84. FILING DATE: 04-OCT-1994
                 MOLECULE TYPE: protein
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STATE: Virginia
COUNTRY: U.S.A.
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ZIP: 22046
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                                    TOPOLOGY:
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301 No. 5989894th Washington Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOLATED DNA CODING FOR SPIDER SILK PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                    US/08/317,844B
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Best Local 9
                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN FIBROUS PROTEIN
                                                                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
               SEQUENCE CHARACTERISTICS:
                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                    CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: HEREWI
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3174 POI CITY: Palo Alto
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                                                                  TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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amino acids
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Best Local Similarity
Matches 238; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08209747 Patent No. 5733771
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IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 1174414
                                                                                                                                COUNTRY: UŚA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin-Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
            ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT., GETALG M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Silk Proteins NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Colgin, Mark
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ELECOMMUNICATION INFORMATION:
                                                                                APPLICATION NUMBER: US/08/209,747
FILING DATE: 14-MAR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                 ADDRESSEE: Birch, Sta
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
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59.2%;
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                  1447-104P
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                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: Lewis,
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ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: N. clavipes TISSUE TYPE: minor am
                                                                                                                                      NUMBER OF SEQUENCES: 5
                                                                                                                                                                     APPLICANT: Colgin, Mark
TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
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                                                                           ADDRESSEE: Birch, St. STREET: P.O. Box 747 CITY: Falls Church STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 GQGAGAAAAAAAAAGGAGQGGYGGLGSQGT-----SGRGGLGGQGAGAAAAAA 108
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                                                            COUNTRY:
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                                                                                                                                                                                                              Lewis, Randolph V.
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                                                                                                                        Stewart, Kolasch & Birch
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pred. No. 1.1e-47;
pred. No. 1.7: Mismatches 97;
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Best Local S
Matches 168
Sequence 3, Application US/08864038A Patent No. 6001592
GENERAL INFORMATION:
APPLICANT: Kunio NAKASHIMA et al
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INFORMATION FOR SEQ ID NO:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 703-205-8050
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FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
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REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-104P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: N. clavipes
TISSUE TYPE: minor ampullate gland
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les 168; Conserv
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                                                                                                                                                                     GLGSQGT-----SGRGGLGGQGAGAAAAAAAAAGGAGQGGYG
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                                                                                                                                                                                                                           AAA--GAGAGGYGGQGGYGAGAGAGAAAAAATGAGGAGGYGRGAGAGAGAAAAGAGAGTGG 491
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 NAKASHIMA et al.
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; LOCATION: from 1 to 73
; IDENTIFICATION METHOD:
US-08-864-038A-3
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Best Local
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TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO: 3
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-5610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/864,038A FILING DATE: May 28, 1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                100
                                                                                                                                                                 233
                                                                                                                                                                                                                                                                                                                                11 GSMASGRGGLGGQGAGAAAAAAAAAAGGAGQ-------GGYGGLGSQGTSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                             TSGRGGLGGQGAGAAAAAAAAAA.
                                                                                                                              GGAGQGGYGGLGSQGTSGRGGLGGQGAG------AAAAAAAAAAGGAGQGGYGGLGSQG 203
                                                                                                                                                                                 --GAGAAAAAAAAAGGAG-----QGGYGGLGSQGTSGRGGLGGQG--AGAAAAAAAAAA 150
                                                                                                                                                                                                                                LGGAAAAAAAAAAAGGAGGLGGLGGLGGLGG-GLGGLGGLGGYGGSAAAAAAAAA
                                                                                                                                                                                                                                                                                               ------RGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQ 99
                                                                                                                                                                                                                                                                                                                                                                al Similarity
167; Conserv
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                                -GGGGGAGAAAAAAAAAASASASRQMSGIRDALGDIKDLLRSNGASAKASAKASAVA 400
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from 1 to 738
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CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBOD
TO SAID POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microsoft Windows
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                                                                                                                                                                                                                                                                                                                                                             Score 593.5; DB 3;
Pred. No. 3.2e-41;
10; Mismatches 82;
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-GGAGQGGYGGLGSQGTSGR---
                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                Indels 147;
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US-08-529-1908-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US08/522,
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathle
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Masucc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE95
FILING DATE: 10-APR-1995
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Masucci, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 617-345-9100
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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STREET: C...
STREET: C...
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200 GSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAA 259
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                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                80
                                                                                                                                                                                                                                    22 GQGAGAAAAAAAAAGGAGQ-GGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 0211
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                                                                                                                                                              GGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGA 139
                                                                                      GAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGL 199
                                                                                                                            AALAAAGAGGGLGGGGGGALAAALAAA-GAGGGGFGGLGGLGGLG 505
                                                                                                                                                                                                                                                                           133;
                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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01-SEP-1995
                                                                                                                                                                                                                                                                                       37.8%;
51.2%;
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GLYCINE-CONTAINING SEQUENCES
CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
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                                                                                                                                                                                                                                                                                       Score 561; DB 2
Pred. No. 5e-39;
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                                                    -GAGGAGGAGAG-GAGAGGAGGAGGAGG-
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                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS LENGTH: 595 amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                   265 GQQGPSGPGSAAAAAAAAAAGPGGYGPGQQGPGGYGPGQQGPSGAGSAAAAAAAGPGQQGL 324
                                                                                                                                                                             147 GPGGYGPGQQGPSGPGSAAAAAAAAASGPGQQGPGGYGP-GQQGPGGYGPGQQGPSGPGSA 205
194 GGYGGLGSQGTSGRG----GLGGQGAGAAAAAAAAA-GGAGQGGYGGLGSQGTSGRG--
                                                                                                                                           103 AAAAAAAAAAGGAGQGGYGGLGSQGTSGRG----GLGGQGAGAAAA------
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FILING DATE: 19-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                   51 GTSGRG----GLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG----GLGGQGAG 102
                                                                                                                                                                                                                                                       87 GGYGPRQQGPGGYGQGQQGPSGPGSAAAASAAASAESGQQGPGGYGPGQQGPGGYGPGQQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                         3 GSHHHHHHGSMASGRGGLGGQGAGAAAAAAAAAAAAAGGAGQ----GGYG------GLGSQ
                                                                                                           AAAAAAASGPGQQGPGGYGP-GQQGPGGYGPGQQGLSGPGSAAAAAAAAGPGQQGPGGYGP
                                                                   -----AAAAAAAGGAGQGGYG-GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQ 193
                                                                                                                                                                                                                                                                                                                              166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595 amino acids
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                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                          37.3%;
44.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205-8000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1447-106P
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Pred. No. 4.1e-38;
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Indels

94; Gaps

17;

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246

264 144

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TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
STATE: Virginia
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Length 595
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US-08-317-844B-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 Aminimum
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Best Local Similarity
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                                                                                                                                                                                                                                   Matches 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NIMBER: 18,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22046
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
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                                  103 AAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG----GLGGQGAGAAAA------ 144
                                                                          147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                              51
                                                                                                                                                    87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                            w
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                                                                          GPGGYGPGQQGPSGPGSAAAAAAAAASGPGQQGPGGYGP-GQQGPGGYGPGQQGPSGPGSA 205
                                                                                                            GTSGRG----GLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG----GLGGQGAG 102
                                                                                                                                                    GGYGPRQQGPGGYGQQQQGPSGPGSAAAASAAASAESGQQGPGGYGPGQQGPGGYGPGQQ 146
AAAAAAASGPGQQGPGGYGP-GQQGPGGYGPGQQGLSGPGSAAAAAAAAGPGQQGPGGYGP
                                                                                                                                                                                            GSHHHHHHGSMASGRGGLGGQGAGAAAAAAAAAAGGAGQ---GGYG-----GLGSQ 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22046
                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08317844B
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                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                   37.3%; Score 554; DB 2; 44.1%; Pred. No. 4.1e-38;
                                                                                                                                                                                                                                   15; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1447-105P
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                                                                                                                                                                                                                                                                     Length 595;
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Best Local
                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ferrari, Fig. 1989.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
TITLE OF SEQUENCES: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-NOV-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/609,716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 YAPGQQGPSGPGSAAA 458
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                                   130 GRGGLG---GQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAA 186
                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Rowland, Bertram I REGISTRATION NUMBER: 200 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Four Embarca
CITY: San Francisco
STATE: CA
                                                                                                                 71
                                                                                                                                                   11 GSMASGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAA 70
                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                 GSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 130
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                                                                       AAAAG-GAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTS 129
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                                                                                                                                                                                         35.0%; Score 520; DB 1; ilarity 43.9%; Pred. No. 4.1e-35; Conservative 22; Mismatches 128
                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -AAAAAAGGAGQGGYG-GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQ
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                                                                                                                                                                                             22; Mismatches 128; Indels
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                                                                                                                                                                                                                               Length 1177;
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                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-175-155-29
                                                                                                                                                                                                                                            Query Match 35.0%; Score 520; DB 1; Best Local Similarity 43.9%; Pred. No. 4.1e-35; Matches 122; Conservative 22; Mismatches 128
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Patent No. 5641648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Ferrar
APPLICANT: Cappel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55186-5/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dorman, Mary A.
TITLE OF INVENTION: Methods for Preparing Synthetic TITLE OF INVENTION: Repetitive DNA
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191
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191
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                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                        71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 29-DEC-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Four Embarca
CITY: San Francisco
                                                                                                                                                                                                      11 GSMASGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                             GAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 250
                                    GRGGLG---GQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG-GAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGR 245
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                                                                               SGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS
                                                                                                                    AAAAG-GAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTS 129
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Crissman, John W.
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11 GSMASGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAA 70

GSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 130

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                                                                                                          ; MOLECULE TYPE: peptide US-08-477-509B-64
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  Matches
                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08,
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPETWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,509B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dorman, Mary A TITLE OF INVENTION: NO. 5770697el Peptides Comprising Repetitive TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same NUMBER OF SEQUENCES: 112
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 06/927,258 FILING DATE: 04-NOV-1986 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/114,618 FILING DATE: 29-OCT-1987 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-JUN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                TOPOLOGY:
                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                            NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGA 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64, Application US/08477509B
o. 5770697
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Crissman, John w
  Conservative
                                                                                                                                                linear
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                      35.0%; Score 520; DB 1; 43.9%; Pred. No. 4.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 08/053,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 08/175,155
                                                                                                                                                                                                                                                          64:
  22; Mismatches 128;
                                     Length 1177;
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
TITLE OF INVENTION: REPETITIVE DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 09-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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                                                                                                                                                                                                                                                                                                      FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                              REGERENCE/DOCKET NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-10/WHD PROCEDER ON THE NUMBER OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/707,237A FILING DATE: 03-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
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                                                             TELEFAX:
                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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Capello, Joseph
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                                                                         (415) 398-3249
                                                                                                              (415) 781-1989
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ID NO:
                                                                                                                                                                                                                                                                 Richard F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 07/114,618
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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LENGTH: 1177 amino aci
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APPLICANT:
                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
FILING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cappello, Joseph APPLICANT: Crissman, John W. APPLICANT: Crissman, John W. TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encod: NUMBER OF SEQUENCES: 112
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                                                                                                                                                                                                        SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 AGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 348
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STRANDEDNESS: un
TOPOLOGY: unknow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 GSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 130
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                                                                                                                                               APPLICATION NUMBER: FILING DATE: 07-JUN CLASSIFICATION: 435
                                   APPLICATION NUMBER: US 0 FILING DATE: 29-OCT-1987
                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                             STREET: Four Embarca
CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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Chambers, James
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our Embarcadero Center,
NUMBER:
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US 08/053,049
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Pred. No. 4.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                 Albritton & Herbert
Suite 3400
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FILING DATE: 22-APR-PRIOR APPLICATION DATA:

22-APR-1993

us 08/175,155

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Best Local Similarity
Matches 122; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,411A
FILING DATE: 07-JUN-1995
                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Flahr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Functional Recombinantly Prepared TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ferrari, Franco A. APPLICANT: Cappello, Joseph
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TOPOLOGY: linear
CLASSIFICATION:
                                                                                                                                                                                      ZIP: 9411
                                                                                                                                                                                                   COUNTRY:
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REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 04
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 06-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
311 AGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAG
                                246 GGLG-GQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSG
                                                                                                                                              130 GRGGLG---GQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAA
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK
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                                                                                          AAG-GAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGR
                                                                       AAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGA
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29-OCT-1987
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43.9%;
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348
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Search completed: July Job time: 517 sec Ψ 2001, 14:56:27

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Result
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
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Match
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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1 MRGSHHHHHGSMASGRGGL.....YGGLGSQGTSGIRRPAAKLN 291
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7777777777777799	837	606	594	783	532	591	615	1011	741	496	694	498	618	396	291	6
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glycine-rich glycine-rich glycine-rich hypothetical	E70835	H70816	G70545	E70824	F70580	B70523	н70589	F70620	G70917	H70839	F70868	C70720	A70989	T49109	S31415	- 10024
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ALIGNMENTS

RESULT A36068

Qy 260AAAAAGGAGQGGYGGLGSQG 279	Qy 221AAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAA 259	Qy 183 220	Qy 136 GQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAA 182 	Qy 97 GGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLG 135	Qy 46 GLGSQGTSGRGGLGGQGAGAAAAAAAAGGAGQGGYGGLGSQGTSGRGGL 96 :	Qy 11 GSMASGRGGLGGQGAGAAAAAAAAAAGGAGQGGYG 45 :	Query Match 68.4%; Score 1015; DB 2; Length 718; Best Local Similarity 59.2%; Pred. No. 1.2e-53; Matches 238; Conservative 8; Mismatches 14; Indels 142; Gaps 13;	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-718 (2UA> A;Cross-references: GB:M37137; NID:g159711; PID:g159712 A;Note: the authors translated the codon GGT for residue 292 as Gln, GTA for residue	R;Xu, M.; Lewis, R.V. Proc. Natl. Acad. Sci. U.S.A. 87, 7120-7124, 1990 A;Title: Structure of a protein superfiber: spider dragline silk. A;Reference number: A36068; MUID:90384959 A;Accession: A36068	A36068 major ampullate fibroin protein - orb spider (Nephila clavipes) (fragment) C;Species: Nephila clavipes C;Date: 08-Mar-1991 #sequence_revision 13-Jan-1993 #text_change 09-Sep-1997 C;Accession: A36068

RESULT

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nuclear antigen EBNA1 - human herpesvirus 4
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Cate: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 22-Oct-1999
C;Accession: C43043; S42440; A03773; S33021
C;Accession: C43043; S42440; A03773; S33021
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1993
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Bar A;Accession: C43043
A;Reference number: A93065; MUID:85035713
A;Accession: C43043
A;Molecule type; DNA
A;Residues: 1-641 <BAN>
A;Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24816.1; PID:g1334880
A;Cross-references: EMBL:V01555; NID:g59074; Deininger, P.L.; Farrell, P.J.; Gibson, Nature 310, 207-211, 1984
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C;Species: Antheraea pernyi (Chinese oak silkmoth)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T31328
R;Sezutsu, H.: Tamura, T.: Yukuhiro, K.
submitted to the EMBL Data Library, August 1998
A;Description: Characterization of the full length fibroin gene of a wild si
A;Reference number: 220995
A;Accession: T31328
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A; Residues: 1-2639 <SEZ>
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nes 174; Conserv
  DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGSDSAAAAAAAAAAAAAAAGSGAGGAGGGYGWGDGGYGSYSAAAAAAAAAAAAAAAGSGAGGRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----QGAGAAAAAAAAAGGAGQGGYGGLGS-------QGTSGRGGLGG 212
sequence and
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39.8%;
expression
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Pred. No. 8.8e-30;
0; Mismatches 90
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of
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416

AGGAGGYGGQGGNAIAGGINGSGGAGGTGGQGGAGGMGGSGADNASGIGADGGAGGTGGN 475 ASGRGGIGGQGAGAAAAAAAAAGGAGQGGYGGIGSQGTSGR------GGIGGQGAG 64

-GGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAG-QGG 119

14

Best Loc Matches

Local Similarity les 140; Conserv

Conservative

37.5%; Score 556.5; DB 2 44.9%; Pred. No. 2.8e-26; tive 13; Mismatches 112

112; DB 2;

47;

Gaps

14;

Length 1901; Indels

Query Match

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A;Reference number: A03794; MUID:84270667
A;Contents: annotation; protein coding region
A;Contents: A; Hummel, M.; Braun, D.; Birkenbach, M.; Kleff, E.
Proc. Natl. Acad. Sci. U.S.A. 83, 5096-5100, 1986
A;Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins:
A;Reference number: S42440; MUID:86259739
A;Accession: S42440
A;Gene: Rv3508
C;Superfamily: collagen alpha 1(IV) chain
                                                                                                                                                                                           A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, A;Title: Deciphering the biology of Mycobacterium tuberculosis from the co A;Reference number: A70500; MUID:98295987
A;Accession: F70806
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                                                           C; Genetics:
                                                                                   A;Cross-references: GB:AL022022; GB:AL123456; A;Experimental source: strain H37Rv
                                                                                                                           A; Molecule type: DNA
A; Residues: 1-1901 <COL>
                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Davilin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                             hypothetical glycine-rich protein Rv3508 - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: F70806
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A; Residues: 1-66 <SAM>
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                                                                                A; Experimental source:
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Pred. No. 8.2e-30;
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                                                                                                      NID: g3261554;
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                                                                                                        PIDN:CAA17745.1; PID:g292
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hypothetical glycine-rich protein Rv3514 - Mycobacterium tuberculosis (strain H37 C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: D70807 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987 A;Accession: D70807
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C;Superfamily: collagen alpha 1(IV) chain
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                                                                                                                                                        AAAAAAGGA------GQGGYGGLGSQG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGGLGSQGTSGI 283
       GGAGQGG----YGGLGSQGTSG 282
                                                             AAAAAAGGAGGGGGGCLGSQGTSGRGGLGGQ----GAGAAAAAA-------AAAA 264
                                                                                                                                                                                                GAAGAGGAAGTGGTGGMIGTTGNAGVGGAGGQGGDGGAGGAGADADQPGATGGTGFA
                                                                                                                                                                                                                                   AAAAAAAAAGGAGQGGYGG-LGSQGTSGRGGLGGQ------GAGAAA------A 182
                                                                                                                                                                                                                                                                                                                                                GKGGVGGVAGLGGAGGAAGQLFSASGAAGNAGVGGAGGQG--GDGGAGGAGADADQPGAT 409
                                                                                                                                                                                                                                                                                                                                                                      GGALGGTGGTGGAGGAGGRGALLLGAGGQGGLGGAGGQGGTGGAGGDGVLGGVGGTG
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                                         GAGGAGGAAGTGGTGGMTGTTGNAGVGGAGGQGGDGGAGGAGADADQPGATGGTGFAGGA
                                                                                                                  GGAGGAGGAGGSSGAGGTNGSGGAGGTGGQGGAGGAGGAGADNPTGIGGTGGDGGTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGGAGGAAGTGGTGGVVGAAGKAGIGGTGGQGGAGGAGSAGTDATATGATGGTGFSGG
                                                                                                                                                                                                                                                                                                             -----GAAAAAAAAAGG-----AGQGGYGGLGSQGT---SGRGGLGGQGAGA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 556; DB 2;
Pred. No. 2.5e-26;
7; Mismatches 103;
                                                                                                                                                        ---TSGRGGLGGQGAGAAAA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 112;
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                                                         RESULT 7

E70806

C; Species: Mycobacterium tuberculosis (strain C; Species: Mycobacterium tuberculosis (strain C; Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C; Accession: E70806
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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Best Local Similarity
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R;Hinman, M.B.; Lewis, R.V.
submitted to the EMBL Data Library, May 1992
A;Description: Isolation of a clone encoding a second dragline silk fibroin: Nephila A;Reference number: $27824
A;Accession: $27824
A;Accession: $27824
A;Accession: $27824
A;Residues: 19-627 <HI2>
A;Cross-references: EMBL:M92913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-627 <HIN>
A;Cross references: GB:M92913; NID:g159713; PID:g159714
A;Note: sequence extracted from NCBI backbone (NCBIP:113893)
R;Hinman, M.B.; Lewis, R.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Hinman, M.B.; Lewis, R.V.
J. Biol. Chem. 267, 19320-19324,
A;Title: Isolation of a clone en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spidroin 2, dragline silk fibroin - orb spider (Nep
N;Alternate names: silk fibroin, dragline
C;Species: Nephila clavipes
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993
C;Accession: A44112; S27824
                                                                                                                                                                                                                                                                                                                                                                                      103 AAAAAAAAAAGGAGQGGYGGLGSQGTSGRG----GLGGQGAGAAAA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2, dragline silk fibroin - orb spider (Nephila clavipes) (fragment)
                                                                                                                                          GGYGGLGSQGTSGRG----GLGGQGAGAAAAAAAAA-GGAGQGGYGGLGSQGTSGRG--
SAAAAAAAAAGPGGYGPGQQGPGGYAPGQQGPSGPGSASAAAAAAAAAGPGGYGPGQQGPGG
                                                      ------GLGGQGAG-----
                                                                                                             GGYGP-GQQGPGGYGPGQQGPGGYGPGSASAAAAAAAGPGQQGPGGYGP-GQQGPSGPGSA
                                                                                                                                                                                                                       GQQGPSGPGSAAAAAAAAAAGPGGYGPGQQGPGGYGPGQQGPSGAGSAAAAAAAGPGQQGL
                                                                                                                                                                                                                                                       -----AAAAAAGGAGQGGYG-GLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQ
                                                                                                                                                                                                                                                                                                                                     AAAAAAASGPGQQGPGGYGP-GQQGPGGYGPGQQGLSGPGSAAAAAAAGPGQQGPGGYGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGYGPRQQGPGGYGQQQQGPSGPGSAAAASAASAASAESGQQGPGGYGPGQQGPGGYGPGQQ 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.3%; Score 554; DB 2; ilarity 44.1%; Pred. No. 1.7e-26; Conservative 15; Mismatches 101
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ne encoding a second
MUID:92406876
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                                                         ----AAAAAAAAAAG----GAGQGGYGG
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D.;

Holroyd,

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Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.;
A;Title: Deciphering the biology of Mycobacterium
A;Reference number: A70500; MUID:98295987
A;Accession: E70806
A;Gene:
C;Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: Rv3507
C;Superfamily: collagen alpha 1(IV)
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A; Cross-references: GB: ALO22022; GB: AL123456; A; Experimental source: strain H37Rv
                                                                                                                                                   A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: B70807
                                                                                                                                                                                                                                 Rajandream, M.A.; Rogers, Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                              hypothetical glycine-rich protein Rv3512 - Mycobacterium tuberculosis (strain c;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: B70807
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                                                      A; Molecule type: DNA
A; Restdues: 1-1079 <COL>
A; Croos-references: GB:AL022022; GB:AL123456;
A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                           R;Cole, S.T.; Brosch, R.; Connor, R.; Davies, R.;
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                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown;
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Best Local Similarity
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                  Rv3512
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                                                                                                                                                                                                                                                       J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                         Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H
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  fibrillar
                                                                           NID: g3261554;
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collagen
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                                                                                                                                       translation not shown
                                                                             PIDN:CAA17749.1;
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  carboxyl-terminal homology
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Accession: H70846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANGIAGNGGDGGDGAAGAVGISGATGAGDGGHGGTGAAGGNGGTGGAGGSGIDGVGGGTG 276
                                                                                                                                                                                                                                                                                                                                                                                        GTGGNGGNGAIGGAGGDAGGSGNSGGNGGIGGKGGNAGAGGAAGSNGGTVGANGTGGDGG
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                                                                                                                               GAGGAGGTGGNGGNITGGTAGTAGAAGNGGAAGKGGAGGQGGTGGGTGGQGGAG
                                                                                                                                                                                            AGAASSATNGGSGGAGGTGGDGGSGGAGGTGGAGGTGGAAGDGGQGGQGGAGG-GAGGQG
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                                                                                                                                                                                                                                                                                                                                                        -AGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQG-----AGAAAAAAAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                 -----AGAAAAAAAAAAAGGA-GQGGY-GGLGSQGTSG
                                                                                                                                                                                                                           -GSQGTSGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRG
                                                                                                                                                                                                                                                                                          -QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.7%;
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H/0846
hypothetical glycine-rich protein Rv3345c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: H70846
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Accession: H70846
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1538 <COL>
A;Experimental source: Strain H37Rv
C;Genee;Cs:
A;Genee; Rv3345c
C;Superfamily: collagen alpha 1(IV) chain

Š 밁 밁 Š В Š 밁 δÃ δÃ Matches Query Match Best Local 1030 1208 1150 1090 VGGVGGAGGDGGAGGVGGFGGQGGIGGEGRTGGNGGSGGDGGGGISLGGNGGLGGNGGVS 1149 165 71 AAAAGGA----GQGGYGGLGSQG-----TSGRGGLGGQGAGAAAAAAAAAAAAGG----11 GSMASGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAA VGLGGDAGSGGAGGNGGIGTDAGGAGGAGGAGGNGGSSKSTTTGNAGSGGAGGNGGTGLN 1267 GMINGGLGGFGGAGGGAYDVAATTGGAGGNGGAGGFASTGLGGPGGAGGPGGAGDFASG 1089 ETGFGGAGGNGGYGGPG--GPEGNGGLGGNGGAGGNGGVSTTGGDGGAGGKGGNGGDGGN 1207 -----AGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQ---Similarity ---GTSGRGGLGGQGAGAAAAAAAAAAGG-------AGQGGYGGLGSQGTS Conservative 36.2%; -AAAGGAGQGGYGGLGSQGTS-GRGGLGGQGAGAAAAAAA 13; Score 538; DB 2; I Pred. No. 2.9e-25; 3; Mismatches 131; Length 1538; Indels 54; Gaps 261 205 164 70 9

Query Match

68

Score 543

5,

DВ

2

Length

1079;

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hypothetical glycine-rich protein Rv2490c - Mycobacterium tuberculosis (strain c;Speckes: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: A70869
C;Accession: A70869
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Haaris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                               RESULT
A70869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987
A; Accession: A70812
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squres, R.; Sulaton, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Deviin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical glycine-rich protein Rv0833 - Mycobacterium tuberculosis (strain c;Speckes: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: A70812
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C;Superfamily: elastin
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A; Residues: 1-749 <COL>
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                                                                                                                                                                                                                                                                                                NGGNGGSGGTSVATGGAGNGGAGGAG--GGAGL 332
                                                                                                                                                                                                                                                                                                                                                                                                                        GGLGGQ-----GAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGQGNHTGGHGGAGGSAGLLALGDGGAGGAGGAATTGTGGAGGAGGKAGLLFGSGGAGGS
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                                                                                                                                                                                                                                                                                                                                                                                  GGAAGTFGDTGNSGGAGGAGGKAGLLFGSGGAGGSGGAGGFANGSTGGAGGAGGGAGLIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNGGAGGSGAPGAIGGAGGPAGLIGVGGAGGAGGAGGAALLFGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 535; DB 2;
Pred. No. 2.6e-25;
9; Mismatches 123;
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                                                                                       Holroyd,
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A; Reference number: A70500; MUID:98295987
A; Accession: A70869
A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A26099
A; Accession: A26099
A; Moleculo territorio
                                                                                                                                                                                                                                                                                                                                                                                                                             R;Condit, C.M.; Meagher, R.B. Nature 323, 178-181, 1986
A;Title: A gene encoding a no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycine-rich cell wall structural protein - garden petunia
C;Species: Petunia x hybrida (garden petunia)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: collagen alpha 1(IV) chain
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A; Gene: Rv2490c
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                                                                                                                                                                                                                                                                                                                                C; Superfamily: Phaseolus
                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-384 <CON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: A26099
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Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                     Local Similarity
                                                                                                 AAAGGA--GQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAG----QGGYGGLG
                                                                                                                                                                          SMASGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAA 71
GGGGGVGGHGGAGGDAGMNGGGGGTGGQGGNGAAGGAG 1355
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                                      SQGTSGRGGLG----
                                                                                                                                                      SFGRGRGAGGGFGGGAGGGAGGGLGGGGGGAG-----GGGGLGG-GGGAGGGFGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGA-GQGGYGG----LGSQ
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                                                                                                                                                                                                                                                     35.4%;
43.6%;
                                                                                                                                                                                                                                                                                                                                glycine-rich cell wall protein
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                                                                                                                                                                                                                                                                                                                                                                                                                             novel glycine-rich
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                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 525.5; DB 2; Pred. No. 1.7e-24;
                                                                                                                                                                                                                                                     Score 525; DB 1;
Pred. No. 6.3e-25;
                                      -GQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID: g3261507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #text_change
                                                                                                                                                                                                                                                                       Length 384;
                                                                                                                                                                                                                                   Indels
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231
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R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroman, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987
A; Accession: A70896
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical glycine-rich protein Rv1091 - Mycobacterium tuberculosis (stra C:Species: Mycobacterium tuberculosis C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 24-Nov-1999 C:Accession: A70896 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, Parkhill, Parkhill, J.; Garnier, T.; Churcher, C.; Harris, Parkhill, Parkhill, Parkhill, Parkhill, Parkhill, Parkhill, J.; Garnier, T.; Churcher, C.; Harris, Parkhill, Par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-853 <COL>
A; Cross-references: GB:AL021897; GB:AL123456;
A; Experimental source: strain H37Rv
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
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                                                         RESULT
F70963
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C;Superfamily: unassigned
Connor, R.; Davies, R.; Devlin, K.; Rajandream, M.A.; Rogers, J.; Rutter, Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.;
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Best L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSHHHHHHGSMASGRGGLGGQ-GAGAAAAAAAAAAGGAGQGGYGGLGSQG--TSGRGGLG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGAGQGGYGGL-----GSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGLGSQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSTNGGGTGGNGGIGGTGGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAVKGGDGGAAAGTGIAGAGGRGGAGGSGGSGGDGGGGAAGPAGWLFGDGGAGGNGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQGA----GAAAAAAAAAAAAAAA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSGGH----ALLWGAGGAGGNGGSGGTGGAGGSTAGAGGNGGAGGGGGTGGLLFGNGGAG
                                                                                                                                                                                                                                                                                                                                                                                                 -AAGGAGQGGYGGLGSQGTSG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAAAAAAGG-----AGQGGYGGLGSQGTS-----GRGGLGGQGAGAAAAAAAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTS-----GRGGLGGQGAGA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGAGGKGGSGLSGNANGGAGGDSGRGGTG--GAGGEGGAAGLLVGTGGHGGDGGAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.0%;
41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 519.5; DB 2;
Pred. No. 2.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
        Taylor, K.;
                                                      S.; Seeger, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NID: g3256022; PIDN: CAA17207.1;
          Whitehead,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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          Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262
          B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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                                                                                    Holroyd,
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                                                                                                                                                                                                                        H37RV)
                                                                                                                  Gordon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome
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C; Superfamily:
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A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987
A;Accession: F70963
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-778 <COL>
A;Coss = references: GB:280225; GB:AL123456; NID:g3242265; pIDN:CAB02341.1; PID:e26639
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: Rv2634c
C;Superfamily: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 134
689
                                                                                  633
                                                                                                                          194
                                                                                                                                                                     573
                                                                                                                                                                                                           147
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                                                                                                                                                                                                                                                                                                                                                                                                                                 393
                                                                                                                                                                                                                                                                                                                                                                                    67 AAAAAAAAGGAGQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 HGSMASGRGG-LGGQGAGAAAAAAAAAAAAGGAGQGGYGGL--GSQGTSGRGGLGGQGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                            NGTDNSGNGNQTGGNGGPGPAGGYGEAGGYGGQCGLGESLDGNDGTGGKGGAGGTAGTDG
                                                                                                                      GGYGGLGSQGTSGRGGLGGQ-----GAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLG
                                                                                                                                                                  VGGAGGEGLTDGAGTAEGGTGGLGGLGGVGGTGGMGGSGGVGGNGGAAGSLIGLGGGGGA
                                                                                                                                                                                         AAAAGGAG------GGGYGGLGS-QGTSGRGGLGGQGA-----GAAAAAAAAAAAAGGAGQ
                                                                                                                                                                                                                                                     DGG IGGDGNGALGAAGGNGGTGGAGGNGGRGGMLIGNGGAGGAGGTGGTGGGGAAGFAGG
                                                                                                                                                                                                                                                                                                                                          GAGGAGGAGGIGETDGSAGGVATGGEGGDGATGGVDGGVGGAGGKGGQGHNTGVGDAFGG
GTTGGSGGAGGLIGWAGAAGGTGAGGTGGQGGLGGQGGNG
                                                                                  GGVGGTG--GIGGIGGAGGNGGAGGAGTTTGGGATIGGGGGTGGVGGAG--GTGGTGGAG
                                                                                                                                                                                                                                                                                             RGGLGGQGAGAAAAAA--AAAAGGAGQGGYGG--LGSQGTSGRGGLGGQGAGAAA--AAA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134;
                                     GQ--GAGAAA-----AAAAAAAGGAGQGGYGGLGSQGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collagens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 516.5; DB 2;
; Pred. No. 3.3e-24;
14; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                  ------GYGGLGSQGTS------G
                                            282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71;
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                                                                                                                               249
                                                                                                                                                                         632
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                                                                                                                                                                                                                                                              572
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: A70934 RESULT 15
A70934
C; Accession: A70934
C; C; Accession: A70934
C; Result: 17 - Jul - 1998
RESULT 15
Mycobacterium tuberculosis
C; C; Accession: A70934
C; Arcession: A70934
C; A7094
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C; A709 A; Molecule type: DNA A; Residues: 1-1306 <COL> A; Cross-references: GB:AL021942; R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, A;Experimental source: strain H37Rv C;Genetics: A; Status: preliminary; nucleic acid sequence Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Nature 393, 537-544, 1998 not shown; translation NID:g3242298; PIDN:CAA17449.1; Squares, not

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Matches Query Match 905 3 GSHHHHHHGSMASGRGGLGGQGA--GAAAAAAAAAGG-----AGQGGYGGLGSQ----GDHALSGNGA-AGGNGGNGGNGSLRGSGGAGGHGGNGGNASRGMGGDGGTGGAGGNAGQI 963 Similarity 34.6%; Score 514; DB 2; Pred. No. 6.8e-24; 20; Mismatches 125; Length 1306; Indels 36; Gaps 50 13;

Rv0578c

collagen alpha 1(IV) chain

Search completed: July 3, 2001, 14:59:23 Job time: 348 sec

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Result
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ALIGNMENTS

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               Viruses; dsDNA viruses,
Gammaherpesvirinae; Lymp
NCBI_TaxID=10377;
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21-JUL-1986 (Rel.
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PIR; A03773; QOBE31
PIR; S33021; S33021
PDB; IVHL; 23-DEC-96.
TRANSFAC, T00211; -.
Nuclear protein; DNA-binding; T;
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SEQUENCE
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"Crystal structure of the DNA-binding domain of the Epstein-
virus origin-binding protein EBNA 1.";

Cell 83:39-46(1995).

-i- FUNCTION: INVOLVED IN LATENT CYCLE. EBNA-1 FUNCTIONS IN
MAINTENANCE REPLICATION OF EBV EPISOME. TRANSACTIVATING
FOR THE ORIGIN AND ENHANCER FUNCTIONS OF ORLP.
-i- SUBCELULIAR LOCATION: NUCLEAR. FREE IN THE NUCLEOPLASM,
ASSOCIATED WITH THE CHROMATIN AND HARDLY, IF AT ALL ASSO
                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Gibson T.J., Hatfull G., Hudson G.S.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the Bigney Box Barrel B.G.;
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MEDLINE-96006523; PubMed-7553871;
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86259739; PubMed=3460083;
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"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.

Mycobacterium tuberculosis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Actinobacteriae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@fisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PE-PORS FAMILY PROTEIN RV3508 PRECURSOR.
RV3508 OR MTV023.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YZ08_MYCTU
053553;
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                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL022022; CAA17745.1; HSSP; P19972; 1KVD. TubercuList; Rv3508; -.
                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000084; -. Pfam; PF00934; PE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein;
 536
                                                                                                                                        416
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                                                                                                                                                                       14 ASGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGR-----
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                                                                                                                                      AGGAGGYGGQGGNAIAGGINGSGGAGGTGGQGGAGGMGGSGADNASGIGADGGAGGTGGN 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAGGAGAGGAGAGGAGGGGG----RGRGGSGGRGRGGSGGRGRGGSGGRR
 AGGAGGAGGNTGVGGTNGSGGQG-GTGGAGGAGGAGGVGADNPTGIGGTGGTGGKG--GA
                              YGGL----GSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQ------GGYGGLGSQGTSGR 169
                                                                   AGAGGAGGAAGTGGTGGVVGAAGKAGIGGTGGQGGAGGAGSAGTDATATGATGGTGFSGG
                                                                                                  AAAAAAAAAAAGGAGQGGY----GGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAAAGGAG-QGG 119
                                                                                                                                                                                                            al Similarity
140; Conserv
                                                                                                                                                                                                                                                                                                 1901 AA; 147627 MW;
                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                    1901
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                                                                                                                                                                                                                            37.5%;
44.9%;
                                                                                                                                                                                                                                                                                                                                                                     Repeat;
                                                                                                                                                                                                                          Score 556.5; DB Pred. No. 6.6e-21
                                                                                                                                                                                                                                                                                                                    RV3508
                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PE-PGRS FAMILY PROTEIN
                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                 Signal
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DOMAIN
REPEAT
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                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation of a clone encoding a second dragline silk fibroin Nephila clavipes dragline silk is a two-protein fiber."; J. Biol. Chem. 267:19320-19324(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Araneomorphae; E
NCBI_TaxID=6915;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPD2_NEPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92406876; PubMed=1527052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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                                                                                                            REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272
                                                                                                                                                                                                                                                                                                                                                                               BIO1. Chem. 267:19320-19324(1992).
FUNCTION: THIS SPIDER MAJOR AMPULLATE SILK POSSESSES UNIQUE CHARACTERISTICS OF STRENGTH AND ELASTICITY. IT MAY CONSIST OF PSEUDOCRISTALLINE REGIONS OF ANTIPARALLEL BETA-SHEET INTERSPERSED WITH ELASTIC AMORPHOUS SEGMENTS.
SUBUNIT: MAJOR SUBUNIT, WITH SPIDROIN 1, OF THE DRAGLINE SILK.
                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGAIGTGGTGGAVGSVGNAGIGGTGGTGGVGGAGGAGAAAAAGSSATGGAGFAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGGAG--GNSGV 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lewis R.V.;
                                                                                                                                                                                                                                     AAA29381.1;
1WFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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  CB9B63779B2C594B CRC64;
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Nephila.
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Query Match 37.3
Best Local Similarity 44.1
Matches 166; Conservative

37.3%;

Score 554; DB 1; Pred. No. 4.6e-21;

Length 627; Indels

15;

Mismatches

101;

94;

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.
GRP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRP1_PETHY P09789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _PETHY
                                                                                                                                                                                                                                                                                "A gene encoding a novel glycine-rich structural protein of petuni nature 323:178-181(1986).

-I- FUNCTION: RESPONSIBLE FOR PLASTICITY OF THE CELL WALL (POTENTI-I-SUBCELLIGIAR LOCATION: CELL WALL (POTENTIAL).

-I- MISCELLANEOUS: THIS PROTEIN CONTAINS 67% GLYCINE RESIDUES.

-I- MISCELLANEOUS: 90% OF THE MATURE PROTEIN RESIDUES ARE CAPABLE FORMING A BETA-PLEATED SHEET COMPOSED OF 8 ANTI-PARALLEL STRAN

-I- MISCELLANEOUS: THE GLYCINE-RICH REGION IS COMPRISED OF TWO REL

FAMILIES OF REPEATS, F1 AND F2, EACH REPEAT CONTAINING ABOUT 4
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Condit C.M., Meagher R.B.;
"A gene encoding a novel of
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Magnoliophyta; eudicotyledons; Solanales; Solanaceae; Petunia NCBI_TaxID=4102;
                                                              EMBL; X04335; CAA27866.1; PIR; A26099; A26099. HSSP; P30129; 4DPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petunia hybrida (Petunia)
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 YAPGQQGPSGPGSAAA
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                                               Structural protein;
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GLYCINE-RICH CELL PROTEIN 1.
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                                               Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384
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               STRUCTURAL
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ABOUT 40
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-9829587; PubMed-9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
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P71933;
01-NOV-1997
                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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01-NOV-1997 (Rel. 35, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                    TubercuList; Rv2634c;
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                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDITINE-20330362; PubMed-10871375;

Zhou C.-Z., Confalonieri F., Medina N., Zivanovic Y.,

Yang T., Jacquet M., Janin J., Duguet M., Perasso R.,

"Fine organization of Bombyx mori fibroin heavy chain
Nucleic Acids Res. 28:2413-2419(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                               FBOH_BOMMO STANDARD; PRT; 5263 AA P05799; Q26379; Q17220; Q1-1988 (Rel. 09, Created) 01-OCT-2000 (Rel. 40, Last annotation update) 01-OCT-2000 (Rel. 40, Last annotation update) FIBROIN HEAVY CHAIN PRECURSOR (FIB-H) (H-FI
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Hypothetical protein
SEQUENCE 778 AA; (
                                                                                                                                                              Tsujimoto Y., Suzuki Y.;
Tsujimoto Y., Suzuki Y.;
The DNA sequence of Bombyx mori fibroin gene
"The DNA sequence of Bombyx mori fibroin gene
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
PARTIAL SEQUENCE FROM N.A STRAIN-KINSHU X SHOWA;
                                        surrounding regions.";
Cell 16:425-436(1979).
                                                                                             PARTIAL SEQUENCE FROM N.A. MEDLINE-79211211; PubMed-4
                                                                                                                                                                                                          SEQUENCE OF 1-168 FROM N.A. MEDLINE-80045039; PubMed-498286;
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                                                                                Tsujimoto Y., Suzuki Y.;
                                                                                                                                       Cell 18:591-600(1979).
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                                                                   "Structural analysis of the fibroin
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INSOLUBLE FORMED OF TWO CHAINS: HEAVY AND LIGHT, THAT ARE LINKED BY A DISULFIDE BOND. HEAVY-LIGHT CHAIN ASSEMBLY IS ESSENTIAL FOR THE EFFICIENT INTRACELLULAR TRANSPORT AND SECRETION OF FIBROIN.

INTERCELLULAR TRANSPORT AND SECRETION OF THE DESCRIPTOR (PSG) SECTION OF SILK GLANDS.

SECTION OF SILK GLANDS.

ANTIDARALLEL BETA SHEETS. THE STRANDS OF THE BETA SHEETS RUN PARALLEL TO THE FIBER AXIS. LONG STRETCHES OF SILK FIBROIN ARE COMPOSED OF MICROCRYSTALLINE ARRAYS OF (-GLY-SER-GLY-FIBROIN ARE COMPOSED OF MICROCRYSTALLINE ARRAYS ALTERNATING WITH AMORPHOUS REGIONS.
                                                                                                                                                                         DISULFID DISULFID CONFLICT
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"Specific codon usage pattern and its
structure of silk fibroin mRNA.";
J. Mol. Biol. 203:917-925(1988).
                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Determination of the site of disulfide linkage
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L; V00094; CAA23432.1; -.
V00097; CAA23433.1; -.
L; S74439; AAB31861.1; -.
L; X13869; CAA32076.1; -.
L; M35378; AAA27839.1; -.
GAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQG-----
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Best Local :
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01-OCT-1994 (Rel. 30, Last annotation update)
01-OCT-1994 (Rel. 30, Last annotation update)
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).
Phaseolus vulgaris (Kidney bean) (French bean).
Eukaryotta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids Trabbles; Fabaceae; Papillonnidaes: "Protein protein p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Glycine-rich cell wall proteins in bean: gene structure association of the protein with the vascular system."; EMBO J. 7.3625-3633(1988).
                                                                                                                                                                                                                                                                                                       CHAIN
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SIMILARITY: THE N-TERMINAL SIGNAL ABOUT 60% HOMOLOGY TO THAT OF THE
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B5C4A9B983B43607 CRC64;
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston Taylor K., Whitehead S., Barrell B.G.;
T "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
I Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        010637;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PE-PERS FAMILY PROTEIN RV1325C P
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
  SEQUENCE
                                DOMAIN
                                                                                                                 Hypothetical
SIGNAL
                                                                                                                                                                                                                               EMBL; Z73902; CAA98089.1;
HSSP; P19972; 1KVD.
TubercuList; Rv1325c; -.
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                                                                                                                                                  Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C. E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:337-544(1998).
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006794;
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                                                                                                                                                             STRAIN-CV. COLUMBIA;
MEDLINE-92003708; PubMed-1912511;
Quigley F., Villiot M.L., Mache R.;
Quigley F., Villiot M.L., Mache R.;
"Nucleotide sequence and expression of a novel glycine-rich protein gene from Arabidopsis thaliana.";
gene from Arabidopsis thaliana.";
Plant Mol. Biol. 17:949-952(1991).
-I- FUNCTION: RESPONSIBLE FOR PLASTICITY OF THE CELL WALL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRP_ARATH P27483;
                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN PRECURSOR
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P41140; 2SFA.
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34; Conservative
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                                                                                                                                                                                                                                                                                                                                                    Brassicaceae; Arabidopsis
 CAA41249.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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74354
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Pred. No. 4.3e-18;
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WAG22 ANTIGEN
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                                                                                                                                  MEDLING-9825987; PubMed-9634230;

A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Oliver S., Osborne J., Ouail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E. Taylor K., Whitehead S., Barrell B.G.;

Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:337-544(1998).

"Control of the MYCOBACTERIAL PE FAMILY; PGRS STMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY; PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P301;
Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV0747 PR
RV0747 OR MTV041.21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y747_MYCTU
O53810;
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                     Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S17732; KNMU.
; P30129; 4DPV
                                                                                                                          SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGLGGGAGGGGGIGGGAGGGLGGGAGGGLGGGHGGGIGGGAGGGAGGGLGGGHGGG
                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration -
sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSG
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338 /
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Pred. No. 3.8e
10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              801
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.8e-18
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|-GAGGGHG
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                                                                                                                                                                                                                                                                                                               Harris
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Best Local
                                                    MEDIINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekkaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekkaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00934; PE; 1.
Hypothetical protein; Repeat;
SIGNAL 1 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TubercuList; Rv0747;
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                                                                                                                                                                                                                                                                               Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV1818C.
                                                                                                                                                                                                                                                                                                                                                                                                     Q50615;
01-NOV-1997
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                                                                                                                                                                                                                                       STRAIN-H37RV;
                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                           RV1818C OR MTCY1A11.25C
                                                                                                                                                                                                                                                                                                                                                                                                                                    YI18_MYCTU
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                           SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGG----LGSQGTSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                              TO THE
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                                            INTEGRAL
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Pred. No. 6.3e-18;
4; Mismatches 120
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POTENTIAL.
HYPOTHETICAL PE-PGRS FAMILY
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                             SRAL MEMBRANE I
MYCOBACTERIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                     498
                                                                                                                                                                                                                                                                                                                 Actinobacteridae;
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                                PROTEIN (PO
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                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                    Mycobacterium.
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ELS_MO
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Hypothetical protein; T
TRANSMEM
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
NCBI_TaxID=10090;
[1]
                                                                                   ELS_MOUSE
P54320;
01-OCT-1996
01-OCT-1996
01-OCT-1996
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                                                Mus musculus (Mouse)
                                                                        ELASTIN PRECURSOR
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HSSP; P19972; 1KVD.
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                                                                                                                                                                                             GNAGSGTPNGSAGTGGAGGLLGKNGMNGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSMASGRGGLGGQGA-----GAAAAAAAAAAGGAGQGGYGGLGSQGTS-----GRGGLG 59
                                                                                                                                                                                                                    AAAAAAAAAGGAGQGGYGG-LGSQGTSGI 283
                                                                                                                                                                                                                                            AGGAGGFGFGGAGGAGGLGGKAGLIGDGGDGGAGGNGTGAKGGDGGAGGGAILVGNGGNG
                                                                                                                                                                                                                                                                    RGGLGGQGAGAAAAAA--AAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGA-----
                                                                                                                                                                                                                                                                                            GGAGGYGST-TGGAGGAGGNAGLLYGAGGAGGAGGALGGGATGYGGAGGNG--GTAGLLFG
                                                                                                                                                                                                                                                                                                                   GGYGGLGSQGTSGRGGLGGQ-----GAGAAAAAAAAAAGGAGQGGYGGLGSQGTS---
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                                                                                                                                                                                                                                                                                                                                                                                                                  GQGAGAAAAAAAAAGG-----AGQGGYGGLGSQGTS------GRGGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                           132;
                                                                      (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 34, Last annotation updat
CURSOR (TROPOELASTIN).
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                                                                                                                                   STANDARD;
                        Chordata;
Rodentia;
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59 POTENTIAL.
13 POTENTIAL.
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Pred. No. 5.3e-18
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4F6F78F2482586BA CRC64;
                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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Best Local :
                         P56877;
30-MAY-2000
30-MAY-2000
30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:95317; Eln.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95130069; PubMed=7829060; Wydner K.S., Sechler J.L., Boyd C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Lung;
                                                                                                                                                                                                                                                                        706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF EPTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
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SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX
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                                                                                                                                    MYCTU
                                                                                                                                                                                                                                                                                                                       AG----AAAAAAAAAAGGAGQGGYGGLGSQGTSGI
                                                                                                                                                                                                                                                                                                                                                                                FGAGAGVPGFGAGAVPGSLAASKAAKYGAAGGLGGPGGLGGPGGLGGPGGLGGAGVPGRV
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860 AA; 71955
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1 27 POTENTIAL.
                         (Rel. 39, Created)
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                                                                                                                                      STANDARD;
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Pred. No. 4.8e-17;
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HYPOTHET ICAL

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FAMILY PROTEIN RV0278C

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Best Local S
Matches 127
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.
Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).

-1- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY; PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TubercuList; Rv0278c; -.
InterPro; IPR000084; -.
Pfam; PF00934; PE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-H37RV;
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SIGNAL 1 30 POTENTIAL.
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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GGDGGHAGVFGNGGDGGCRR 882
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Search completed: July

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09109 cynomolgus
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O46172;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DRAGLINE SILK PROTEIN SPIDROIN 1 (FRAGMENT).
Nephila clavipes (Orb spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoldea; Tetragnathidae;
                                                                                                                                                                                          SEQUENCE FROM N.A.

Beckwitt R., Arcidiacono S., Stote R.;
Insect Biochem. Mol. Biol. 0:0-0(1998).

EMBL; U37520; AAC04504.1; -.

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SEQUENCE 617 AA; 49410 MW; 1EF0CE92
                                                                                                                                                                                                                                                                                                               proteins (Spidroin) from Nephila clavipes
bicentenarius (Araneidae).";
J. Biol. Chem. 269:6661-6663(1994).
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MEDLINE-94165058; PubMed-8120021;
Beckwitt R., Arcidiacono S.;
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               QGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAA 109
QG-AGRGGSGGQGAG----AAAAAAAGGAGQGGYGGLGSQG-AGRGGLGGQGAGAAAAAAA
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49410 MW; 1EF0CE9269A832E2 CRC64;
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01-JUN-1998 (TrEMBLTel. 06, L)
01-MAR-2001 (TrEMBLTel. 16, L)
SPIDROIN 1 (FRAGMENT).
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Beckwitt R., Arcidiacono S., Stote R.;

Beckwitt R., Mol. Biol. 0:0-0(1998)
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EMBL; U20329; AAC3895
                                                                                                                                                                                                                                      Arcidiacono S., Mello C., Kaplan D., Cheley S., Ba "purification and characterization of recombinant expressed in Escherichia coll.";
Appl. Microbiol. Biotechnol. 49:31-38(1998).
                                                                                                                                                                  Beckwitt
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Xu M., Lewis R.V.;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Spider minor ampullate silk proteins contain new repetitive sequences and highly conserved non-silk-like 'spacer regions'."; Protein Sci. 7:667-672(1998).
EMBL; AF027735; AAC14589.1; -.
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MEDLINE-98200471; PubMed-9541398;
Colgin M.A., Lewis R.V.;
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540
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                                                                                                                                              GAAAAAAAAAAGGAGQGGYGG-------LGSQGTSGRGGLG---GQGAGAAAAAA 222
                                                                                                                                                                                                                          GGLG---GQGAGAAAAAAAAAGGAGQGGYGGLGSQGT------SGRGGLGGQGA 177
                                                                                                                                                                                                                                                                                                                          GQGGYGAGAGAAAAAAGAGAGGAGGYGRGAGAGAGAAAAGAGAGGYGGQGGYGAGAGAGAG 359
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167; Conserv
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Pred. No. 2.4e-39;
6; Mismatches 95
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Best Local Similarity 56.9
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               O76786 PRELIMINARY; PRT; 2639 AA. 076786; O1-NOV-1998 (TremBLrel. 08, Created) O1-NOV-1998 (TremBLrel. 08, Last sequence update) O1-OCT-2000 (TremBLrel. 15, Last annotation update)
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NON_TER
SEQUENCE
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MEDILINE-96178678; PubMed-8600519;

Guerette P.A., Ginzinger D.G., Weber B.H., Gosline J.M.;

"Silk properties determined by gland-specific expression fibroin gene family.";

Science 272:112-115(1996).

EMBL; U47856; AAC47011.1; -.

NON TER
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Q16988;
Q1-NOV-1996 (TIEMBLIEL 01,
Q1-NOV-1996 (TIEMBLIEL 01,
Q1-QCT-2000 (TIEMBLIEL 15,
                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Saturniidae; Saturniinae; Antheraea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Araneus diadematus (Spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Araneidae; Araneus.
NCBI_TaxID-45920;
                                                                                                                                                                                                                                                                                                                                                                                                                                             FIBROIN.
SEQUENCE FROM N.A.
Sezutsu H., Tamura T., Yukuhiro K.;
"Characterization of the full length fibroin
Antheraea pernyi.";
                                                                                                                                                                                                                                                                                                                                                                                                 Antheraea pernyi (Chinese oak silk moth).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGPGGPGSSAAAAAAA--GSGPGGYGP-ENQGPSGPGGYGPGGSGSSAAAAAAAAA--SGP
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%; Pred. No. 2.6e-37;
24; Mismatches 61;
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QY 11 GSMASGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLG	Ouery Match 40.0%; Score 593.5; DB 5; Length Best Local Similarity 41.1%; Pred. No. 7.3e-34; Matches 167; Conservative 10; Mismatches 82; Indels		DT 01-JUL-1997 (TrEMBLrel. 04, Created) DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update) DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) DE INSOLUBLE PROTEIN. OS Pinctada fucata. OS Eŭkaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; E CC Pterioidea; Pteriidae; Pinctada. OX NCBL_TaxID-50426; RN (11_TaxID-50426;	SU 24	Qy 272 YGGLGSQGTSGIRRPAA 288 	Qy 213 QGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAG-GAGQGG ::	Qy 175QGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGG	Qy 137QGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGG	Qy 122	Qy 91	OY 53SGRGGLGGOGAGAAAAAAAAAAGGAGQGGYGGLGSQGT	Qy 14 ASGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGT	Query Match 41.6%; Score 617.5; DB 5; Length Best Local Similarity 39.8%; Pred. No. 4.9e-35; Matches 174; Conservative 10; Mismatches 90; Indels	RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. DR EMBL; AF083334; AAC32606.1; SQ SEQUENCE 2639 AA; 216056 MW; 2EE3310DEEB09B9A CRC64;
GGYGGLGSQGTSG 54 LGGGLGGLGGLGGGGD 172	ength 738; ndels 147; Gaps 12;	uchi K., Tanaka M.,	ia; Pterioida;			AAAAAAG-GAGQGG 271 AAAAAAGSGAGGRG 1561	QTTSGRGGLGG 212 	SGRGGLGG 174 : SGAGGVGGGYGWGDG 1441	GG 136 GGGYGWGDGGYGSD 1381	AGGAGQGGYG- 121 	GGYGGLGSQGT 90 	GLGSQGT 52 YGSDSAAAAAAAA 1201	ength 2639; ndels 163; Gaps 13;	ases. RC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98295987; PubMed-9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Quail M.A., Rajandream M.A., Rogers J., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Squares S., Squares R., Sulston J.E., RA Rutter S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Seeger R., Stelton S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Squares S., Sqares R., Sulston J.E., RA Rutter S., Squares S., Sqares R., Sulston J., Ra Rutter S., Squares S., Sqares R., Sulston J., Ra Rutter S., Squares S., Sqares R., Sulston J., Squares S., Sqares S., Sqares R., Sulston J., Squares S., Squares S.
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Last annotation update)
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RA Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigimeier K., Gas S., Barry C.E. III, Tekala F.,
RA Gordon S.V., Eigimeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badocck K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,
RA Tylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
RI Nature 393:537-544(1998).
DR EMBL, ALO2202; CAA17744.1; -.
DR HSSP, P00778; ZULL.
DR HSSP, P00778; ZULL.
DR InterPro; IPR0020084; -.
DR InterPro; IPR002173; -.
                                                                                                                                   Matches 144;
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053552;
01-JUN-1998 (TrEMBLrel. 0
01-JUN-1998 (TrEMBLrel. 0
01-OCT-2000 (TrEMBLrel. 1
PGRS-FAMILY PROTEIN.
                                                                                                                                                                                                              Pfam; PF00934; PE; 1.
ProDom; PD001223; -; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_2
SEQUENCE 1381 AA; 110624 MW; CA09676BDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
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                                                                                                                                                   Local Similarity
                                                                                   MRGSHHHHHHGSMASGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGL--GSQGTSGRGGL 58
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                              GGQGAGAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAGGA---
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GGQGTGAGGAAGAGGTG--
                                                               MGGTGGNGGNGALLIGGGGLG--GAGGNGGTGGGTGGNGGNGALLIGAGGVGGAGGI
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37.8%;
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                                                                                                                                 ; Score 544.5; DB 2;
; Pred. No. 2.9e-30;
17; Mismatches 115;
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Best Local Similarity 40.7
Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Elglmeter K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RV3512 OR MTV023.19. Mycobacterium tuberculosis.
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NGGAAGAATAGSNGGAGTGSAGGNG--GTGGRGGSGGAGGDGIGGVGGGKGGNGADGEVG 394
                                                         -AGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQG----
                                                                                                                  GTGGNGGNGAIGGAGGDAGGSGNSGGNGGIGGKGGNAGAGGAAGSNGGTVGANGTGGDGG
                                                                                                                                                                         GLGGQGAGAAAAAAAAAGGAG-QGGYGGLGSQ------GTSGRGGLGGQG- 100
                                                                                                                                                                                                                               ANGIAGNGGDGGDGAAGAYGISGATGAGDGGHGGTGAAGGNGGTGGAGGSGIDGYGGGTG 276
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Pred. No. 2.7
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O1-AUG-1998 (TREMBLrel. C
O1-OCT-2000 (TREMBLREL.)
PGRS-FAMILY PROTEIN.
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Q16986;
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Eukaryota; Metazoa; Arthropoda;
Araneomorphae; Entelegynae; Aran
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52.3%;
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Pred. No. 1.2e-30;
9; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -AGGAGQG-----YGAAGLGGQGGAGQGGGSGAA
                                                                                                                                                    PRT;
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PE_PGRS

OR RV3345C OR MTV004.01C-MTV016.45C

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RESULT
O53844
ID O5
AC O5
DT 01
DT 0.0
DT 0.0
GN R
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Best Local S
Matches 126
O53844; PRELIMINARY;
O53844; O1-JUN-1998 (TrEMBLrel. (
O1-JUN-1998 (TrEMBLrel. (
O1-OCT-2000 (TrEMBLrel. )
PGRS-FABILY PROTEIN.
RV0833 OR MTV043.25.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Besham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.; Taylor K., Whitehead S., Barrell B.G.; Complete genome sequence.";
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InterPro; IPR002173; -.
Ffam; PF00934; PE; 1.
ProDom; PD001223; -; 1.
PROSITE; PS00583; PFKB_KINASES_1;
SEQUENCE 1538 AA; 129386 MW; 7
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EMBL; ALO21841; CAA171
HSSP; P00441; 1SOS.
TubercuList; Rv3345c;
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                                                                                                                                                                                                                                                                                                      VVNVTAGHGGNGGNGGNGSAG
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                                                           Last sequence up
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Pred. No. 8.8e
l3; Mismatches
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                                                                                                                 Created)
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3.8e-30;
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"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

RI Complete genome sequence.";

RL EMBL, ALO22004; CAA17639.1;

R Tuberculist: Rv0R33.
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Best Local Similarity 39.9
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                               Q93119 PRELIMINARY; PRT; 421 AA.
Q93119; CTEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence up
01-OCT-2000 (TrEMBLREL. 15, Last annotation
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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  SEQUENCE FROM N.A.
TISSUE-POSTERIOR SILKGLANDS;
Yukuhiro K., Kanda T., Tamura T.;
"Preferential codon usage and two
fibroin gene of the Chinese oak si
Insect Mol. Biol. 0:0-0(1996).
                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glos Bombycoidea; Saturniidae; Saturniinae; Antheraea.
                                                                                                                                                                                                                                                                                                    ANTHERAEA PERNYI FIBROIN (FRAGMENT).
Antheraea pernyi (Chinese oak silk moth)
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Pred. No. 7
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.7e-30;
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                                  Antheraea
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                                        complete genome sequence.";
Nature 393:537-544(1998).
EMBL; AL021246; CAA16067.1;
Tuberculist; RV2490c;
InterPro; IPR00084;
InterPro; IPR000228;
InterPro; IPR00173;
InterPro; IPR00173;
                                                                                                                                                                                                                        Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandram M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the
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Bacteria; Firmicutes; Actinobacteria;
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Q9M3Y2;
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Q1-CT-2000 (TrEMBLrel. 15, Created)
Q1-CT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Magnoliophyta; Liliopsida;
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Ringli C., Hauf G., Keller B.;
"Hydrophobic properties of the structural protein GRP1.8
wall of protoxylem elements.";
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                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2000) to the EMBL; AJ276509; CAB88804.1;
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InterPro; IPR002952; -.
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5; Mismatches
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GLYCINE-RICH PROTEIN GRP1

GEF5E2AA751A8B04 CRC64;
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Search completed: July 3, 2001, 15:05:16 Job time: 581 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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             N. clavipes draglin spider dragline va Polymer of an anal Nephila clavipes s Spider dragline va Polymer of an anal Spider dragline va
                                                                                                                                                                                                                                                              Description
                                                                                                                                                                   Spider silk protei
Nephila clavipės s
N. clavipes spider
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Spider silk protei	AAY40098	20	531	31.6		5
-	AAW01496	16	1018	31.6	1105.5	4
Sequence encoding	AAR05312	1	1066	۲.	1114	Ω
SLPIII	AAW26350	18	1050	2	_	2
SLPIII amino	AAY78286	21	979	2	1127	Ξ
FCB-SLP pro	AAB63997	22	1038	۲.	_	ö
Repetitive protei	AAB72727	22	1038		1129	9
Fibron	AAR95107	17	1038		1129	æ
SLP-C prote	AAB63999	22	1332		1131	3
Repetitive prot	AAB72729		1332	2	1131	8
Sil	AAR95109		1332	32.4	1131	5
	AAY59071		595	2	1132	4
	AAW53347		595		1132	ü
N.clavip	AAR14309		595	2	1132	ະ
New DNA s	AAW56163		738		1157	Ξ.
Adhesion protein.	AAR81318	16	980	ω.	1166	ŏ
protei	AAP82962	φ	1059		\mathbf{H}	
	AAY78283	21	1101	ω	H	8
SLP4 synthetic pro	AAW26348	18	1059	Ψ	_	27
multin	10	14	1059	ω ·	\rightarrow	8
acid	352	19	1023	ω.	176.	5
mino acid	AAW53518	19	1178	5	233.	2
Silk-like protein	Ξ	14	1178	5	1233.5	ິລ
SLPIII protein seg	39	22	1177	5	233.	2
Repetitive protein	AAB72725	22	1177	5	233.	2
	27	21	1177	5	233.	õ
ô	AAW26342	18	1177	5	233.	9
~	_	17	1177	5	233.	8
SLP III (Silk-fibr	053	11	1177	5	233.	7
SlPIII protein com	AAP80940	9	1177		233.	5
an ar	010	20	714	œ	331.	5
line v	9905	16	714	8	331.	4
r silk r	Y4009	20	615	39.9	13	ω
pMISS1 MiSP spider	AAR80168	16	831	0	1405.5	2

ALIGNMENTS

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RESULT
AAY40097
ID AAY4
XX AAY4
AC AAY4
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XX Spid
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XX Spid
XX Spid
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XX Hepl
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XX Hepl
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                                                                                                                                                                                                                             WPI; 1999-510729/43.
                                                                                                                                                                                                                                                                                                            Philippe M, Garson JC,
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Claim 3; Fig 1; 32pp; French.

Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens -

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Best Local S
Matches 495
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                                                                                                                                                                               ggygglgsqgagr---ggqgagaaaaaavgagqegirgqgagqggygglgsqg-sgrggl
                                                                                                                                                                                                              GGYGP-GQQTSGRGGLGGQGAGAAAAAAAAAA-----AGGAGQGGYGGLGSQGTSGRGGL
                                                                                                                                                                                                                                            lgnqg-agrgglggggg----aaaaaaaggagqggygglgnqgagrggqgaaaaaggagq
                                                                                                                                                                                                                                                                                                      ag---avaaaaaggaggggggglgsgg----agrggggag----aaaaaaggagqrgygg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                  ----AAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQG
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                                                                                                                                                                                                 Indels 176;
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20-APR-1990;
04-OCT-1994;
                                                                                                                                                                                                                                                                                                                                The present sequence represents a spider silk protein from the present invention. Spider silk proteins, and peptide fragments within the proteins, can be produced and purified independently and can then be mixed and made into fibres that have higher tensile strengths and elasticity than naturally occurring fibres. The fibres can be used in mixed composites. The invention allows the two naturally occurring Nephila clavipes silk proteins to be produced independently so that they can later be combined to form silk fibres of high tensile strength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW53346 standard; Protein; 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spider;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant spider silk proteins - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hinman MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-1998
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                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                       and elasticity.
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                                                                                                                                                                                                   23 QGAGAAAAAAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGGQGAG-AAAAAAAAAAAGGAGQ
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                                                         AGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAA------AGGAGQGGYGGLG
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                                                                                                         GGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGA
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sqg-agrgglggqgagaaaaaaaggagggglggggagqgagasaaaaggagggggggglgs
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                                             aggagqggygglgsqg-agrgglggqgagaaaaaaggagqggygglggqgagqggygglg
                       SQGTSGRGGLGGQGAGAAAAAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nephila clavipes; silk protein; tensile strength; elasticity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clavipes
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90US-0511792.
94US-0317844.
95US-0425069.
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Pred. No. 1.5e-148;
5; Mismatches 39;
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                         AAAAGGAGQGGYGGLGS
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The invention provides isolated cDNA molecules coding for spider silk proteins. The spider silk proteins are characterized by repeating alpha and beta regions and optional variable regions. The DNA sequences are useful in the production of spider silk protein by recombinant DNA techniques. The recombinant spider silk proteins may be used for the
                                                                                                                                                                                                                                                                                                                                      N. clavipes
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                                                                   Claim
                                                                                                                      N-PSDB; AAZ38195
                                                                                                                                                     Hinman MB,
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20-APR-1990;
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                                                                                                                                                                                                                                                                                                                 Spider silk protein;
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                                                                                    lated DNA, vector and production of spider
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                                     15-JAN-1992
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. No. 1.5e-148;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding spider silk protein-1 and 2 and variants - isolated from Nephila clavipes, for prodn. of spider silk protein and fibres having desired characteristics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
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vaaaaaggagggggglgsqg----agrggggag----aaaaaaaggagqrgygglgnqg-
                                                   aaaaggagggglggggggggagaaaaaaggaggggggglgsgg-agrgglggggag---a
                                                                                                      agrggegag----aaaaaaggaggggggglgggg-aggggygglgsqgagrgglggggag
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Pred. No. 6.7e-148;
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This sequence represents a synthetic spider dragline variant polymer, CC Dp-1A.9. The sequence of the Dp-1A.9 monomer is given in AAR99052. CC The polypeptide monomer is a variant based on a consensus sequence cd derived from the fibre forming regions of spider dragline protein, CC esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. CC DNA sequence encoding the monomer may be used in the recombinant CC production of the variant protein in a recombinant bost, e.g. E. coli CC or Bacillus subtilis. Synthetic analogues of Dp1 were designed to mimic CC of variation among individual repeats. Dp-1A analogues are composed CC of a tandemly repeated 101 amino acid monomer which comprises four repeats which differ from the consensus sequence given in AAW05201, CC residues; (1)-(5) given below. This 101 amino acid monomer is repeated 1-16 times in a series of analogue proteins. The individual repeats of analogue proteins. The conditional repeats differ from the consensus according to the pattern: (2) when the entire poly-alanine sequence is deleted, conditions is the surrounding sequence encompassing AGRGGIGGOGAGANGG: (3) aside from the poly-alanine sequence, deletions usually
                                                                                                                                                                                                                                                                                                                                                  etc., also related DNA, vectors and transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DP-1A
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                                                                                                                                                                                                                                                                                                                        Disclosure; Page 85-87; 168pp;
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                                                                                                                                                                                                                                                                                                                                                               New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encompass integral multiples of three consecutive residues;
(4) deletion of GYG is generally accompanied by deletion of the same sequence; and
in the same sequence; and
(5) a repeat in which the entire poly-alanine sequence is deleted is generally preceded by a repeat containing six alanine
19-NOV-1999
                           AAY40100;
                                                      AAY40100 standard;
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                                                                                                                      AAGGAGOGGYGGLGSQGT--SGRGGLGGQGA---GAAAAAAAAAAGGAGQGGYGGLGSQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAG
                                                                                                                                                                                                        TSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAA 641
                                                                                                                                                                                                                                                                                       aaaaggagqggygglgsqgagrgglggqgagaaaaaaaggagqgglgsqgagqagaaaa
                                                                                                                                                                                                                                                                                                                    AAAAGGAGQGGYGGLGSQGT--SGPGGYGPGQQT----SGRGGLGGQGAGAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGLGSQGTS
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                                                                                                                                                   AGGAGQGGYGGLGSQGTSGPGGYG 665
                                                                                                                                                                             -agrgglggggg---aaaaaaaggagg--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          606 AA;
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(first entry)
                                                     protein;
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                                                                                                                         601
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                                                                                                                                                                            -gg1gsqgagqgagaaaa
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Best Local S
Matches 477
                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a polymer of an analogue of the spider silk protein spidroine major 1. The protein improves the moisturizing/ softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins,
                                                                                                                                                                                                                                                                                                                                                                                                         hormones, moisturizers or agents for treating disorders of skin and hair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscreen; hormone; moisturizer; skin disorder; skin disorder.
                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                          GQGAGAAAAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGGQGA---GAAAAAAAAAAAAAGG
                                                                                                                                                qgagrggqgagaaaaaaggagqggygglgsqgagrgglggqgagaaaaaaaggagqgglg
                                                                                                                                                                QGA----GAAAAAAAAAGGAGQGGYGGLGSQGT------SGRGGLG
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                                                                                                                                                                                                                   QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGG
                                                                                                                                                                                                                                                                                                             cal Similarity
477; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Fig 4B; 32pp; French.
                                                                                                                                                                                                                                                                                                                                                                               606 AA;
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                                                                                                                                                                                                                                                                                                            59.4%; Score 2076; DB 20; 69.7%; Pred. No. 2.5e-144; ative 11; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arraudeau
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AAW27178

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                  A process has been developed for the production of a DNA fragment encoding silk protein. The process involves: (a) selecting target DNA, from a silk-producing spider, that contains many repetitive and non-repetitive regions; (b) selecting a single-stranded DNA primer of at least 10 nucleotides with a sequence that is complementary to a region of the target; (c) repetitively combining the primer with melted target DNA, incubating the mixture with nucleotides and a DNA polymerase with
                                                                                                                                                                               New opt. multimerised DNA sequences encoding spider silk protein contg. both repetitive and non-repetitive sequences, useful for making high strength films, fibres, woven articles etc.
                                                                                                                                                                                                                                                                                                                              (BASE/)
                                                                                                                                                                                                                                                                                                Basel RM,
                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-1996;
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RESULT AAR99055

8

XXX DXX XXX

17-JAN-1997

(first

entry)

AAR99055;

AAR99055 standard; Protein;

606

Spider dragline variant, DP-1B.9 polymer.

dragline

protein;

variant;

monomer;

polymer;

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Matches 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the target and is at least 2 kb long. The present sequence encodes the spider silk protein from Nephila clavipes. The DNA fragment can be used to make fibres, films, woven articles, e.g. for use in parachites, sails, body armour, and absorbers (e.g. of heavy metals, biological weapons, DNA, chemicals, flavours and fragrances). The high molecular weight (90-250 kD) of spider silk proteins can be produced on a commercial scale (at over 2 g/l cell mass). It has better tensile strength and elasticity than silkworm silk. Inclusion of both repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and non-repetitive regions ensures isolation of stable clones.
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GQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAGGAGQGG
                                                                                                                                                                                                                                                                                                                                       GGLGSQGTSGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAA
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                                                                                 SGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAA
                                                                                                                             ygg1ggg-agqggygg1gsqgsgrgg1ggqgag----aaaaaaggagq--
                                                                                                                                                              YGGLGSQGTSGPGGYGP-GQQTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGLGSQGT
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                                                                .gglggqgagqgagaaaaaaggagqggygglgsqg.---agrggqgag----aaaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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71.9%;
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Pred. No. 1.4e-142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                               CC The polypeptide monomer is a variant based on a consensus sequence CC derived from the fibre forming regions of spider dragline protein, CC esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. The CC DNA sequence encoding the monomer may be used in the recombinant CC production of the variant protein in a recombinant host, e.g. E. coli CC or Bacillus subtilis. Synthetic analogues of DP1 were designed to mimic CC the repeating consensus sequence of the natural protein and the pattern CC of variation among individual repeats. This monomer exhibits all of the CC regularities of (1)-(5) below. In addition, it exhibits a regularity of CC the natural sequence which is not shared by DP-1A, namely that a repeat CC in which both GYG and GRC are deleted is generally preceded by a repeat CC in which both GYG and GRC are deleted is generally preceded by a repeat CC a more extended segment than does DP-1A. The individual repeats differ CC a more extended segment than does DP-1A. The individual repeats differ CC (1) the poly-alanine sequence varies in length from 0-7 CC (1) the poly-alanine sequence varies in length from 0-7 CC (1) saide from the poly-alanine sequence varies in length from 0-7 CC (3) aside from the poly-alanine sequence, deletions usually CC (3) aside from the poly-alanine sequence, deletions usually CC (4) deletion of GYG is generally accompanied by deletion of GRG CC in the same sequence; and (5) a repeat in which the entire poly-alanine sequence is decended to the same sequence; and (5) a repeat in which the entire poly-alanine sequence is consecutive residues; (6) a repeat in which the entire poly-alanine sequence is consecutive is deletion of GRG CC deleted is generally preceded by a repeat containing six alanine sequence is consecutive residues.
                                                                                                                                                                                                                                  Matches 462;
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                       Best
                                                                                                                                                                                                                                                                                                                                                                                        The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibre forming region; Spidroin 1; Nephila clavipes; DP1; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope; surgical suture; implant; reinforcement; film; coating.
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 88-90; 168pp; English.
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    158
                                               43
                                                                                          98
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                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a synthetic spider dragline variant polymer, B.9. The sequence of the DP-1B.9 monomer is given in AAR99054.
                                                                                                                                                             GAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLG 97
YGGLGSQGTSGPGGYGP-GQQTSGRGGLGGQGAGAAAA--
                                          sqgagqgagaaaaaaggagqggygg1gsqg----agrggqgag----aaaaaaggagqgg
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                                                                                                                                                                                                                                                                                                                                               606 AA;
                                                                                                                                                                                                                               Conservative
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64.2%;
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                                                                                                                                                                                                                             Mismatches
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           Philippe M,
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                                                                                                                                                                                                                                                                                                                                                                   AAY40102 standard; protein; 606
                                                            11-FEB-1998;
                                                                                   11-FEB-1998;
                                                                                                                                 FR2774588-A1
                                                                                                                                                                     Peptide
                                                                                                                                                                                                                    Synthetic
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                                  (OREA ) L'OREAL SA.
                                                                                                                                                                                                       Nephila clavipes.
                                                                                                                                                                                                                                                                                          Polymer of an
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            Garson
                                                                                                                                                                                                                                                                                          analogue of spider silk protein spidroine major 1.
                                                            98FR-0001614
                                                                                   98FR-0001614
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                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cosmetic
for hair
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agaaaaaaggagqggygglgsqg----agrggqgag----aaaaaaggagqggyggllgsq
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Pred. No. 8.8e-137;
                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                      CC DP-1B.16. The sequence of the DP-1B.16 monomer is given in AAR99056.
CC DP-1B.16. The sequence of the DP-1B.16 monomer is given in AAR99056.
CC The polypeptide monomer is a variant based on a consensus sequence
CC derived from the fibre forming regions of spider dragline protein,
CC esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. The
CDNA sequence encoding the monomer may be used in the recombinant
CC or Bacillus subtilis. Synthetic analogues of DPI were designed to mimic
CC or Tacillus subtilis. Synthetic analogues of DPI were designed to mimic
CC or Tacillus subtilis. Synthetic analogues of DPI were designed to mimic
CC or Tacillus subtilis. This monomer exhibits all of the
CC regularities of (1)-(5) below. In addition, it exhibits a regularity of
CC regularities of (1)-(5) below. In addition, it exhibits a regularity of
CC the natural sequence which is not shared by DP-1A, namely that a repeat
CC in which both GYG and GRG are deleted is generally preceded by a repeat
CC taking the entire poly-alanine repeat, with one intervening repeat.
CC The sequence of DP-1B matches the natural sequence more closely over
CC a more extended segment than does DP-1A. The individual repeats differ
CC from the consensus sequence given in AAM06201 according to the pattern:
CC from the consensus sequence varies in length from 0-7
CC residues; (2) when the entire poly-alanine sequence is deleted,
CC so also is the surrounding sequence more, deletions usually
CC encompass integral multiples of three consecutive residues;
CC in the same sequence, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spider; aray-
fibre forming region, -
fibre;
                                                                                                                                                                                                        in the same sequence; and (5) a repeat in which deleted is generally preceded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR99057 standard; Protein; 604 AA.
   Sequence
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                                                                     for implants, plastic
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                                                                 proteins may be used to produce fibres of high tensile strength and sticity, suitable for clothing, rope, surgical sutures, biomaterials implants, plastic reinforcements, films, coatings, etc.
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Best Local Similarity

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                   Key
Peptide
                                                                               Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscrehormone; moisturizer; skin disorder; skin disorder.
                                                            Synthetic
                                                                                                                        Polymer of an analogue of spider silk protein spidroine
                                                                                                                                                 19-NOV-1999
                                                                                                                                                                   AAY40101;
                                                                                                                                                                                       AAY40101 standard;
                                                   Nephila clavipes.
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                            Location/Qualifiers
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Best Local Similarity
Matches 460; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens \,\cdot\,
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                                                     Query Match
Best Local Similarity
                            Matches
                                                                                                                                                                                                                                     This sequence represents the product of cDNA clone, pMISS1, encoding the orb web spider minor ampullate silk protein MiSP1 has been identified and sequenced. Repeat unit peptides of MiSP1 may form part of a larger polypeptide with an amino terminus (see AAR80184-85) and a carboxy terminus (see AAR80186-89). Repeat unit peptides make up spider silk proteins (spidroins) which in turn aggregate to form the silk fibres have high tensile strength and significant elasticity. An isolated cDNA clone of a silk protein encoding sequence is of use to produce the protein at high yields
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide(s) comprising repeated unit amino acid sequences, cDNAs - derived from minor ampullate spider silk proteins and to form spider silk fibres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pMISS1 MiSP spider silk protein insert product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1996
                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 1; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9525165-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spider silk; repeat unit; consensus; minor ampullate spidroin; MiSP; orb web spider; dragline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR80168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYWY-) UNIV WYOMING
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                                                                                                                                                                                                                       recombinant DNA technology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis RV;
                                                                                                                                                                 831 AA;
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                                                     Score 1405.5; DB 16; Pred. No. 2.2e-95;
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                                                                                                                                                                                                                                                                                                   Spider silk protein; spidroine minor 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscrehormone; moisturizer; skin disorder; skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                               Spider silk
                            11-FEB-1998;
                                                                                  11-FEB-1998;
                                                                                                                                        13-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         grgagagagaaagagagtgg-----agyggggggggagagagaaaaagagaggagyg
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                                                                                                                                                                                                                                                                                                                                                                                                               protein
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                            98FR-0001614
                                                                                  98FR-0001614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                               spidroine
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                                                                                                                                                                                                                                                                                                                                                                                                                  minor 1.
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                                                                                                                                                                                                                                                                                                                                sunscreen;
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449

470

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682 615 637 555 577 340

353

412

293

286

241

183

129 80

(OREA) L'OREAL

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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the natural spider silk protein spidroine minor 1. The protein improves the moisturizing/softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make up or sunscreens. As the protein is a good, persistent fillm-formers on the skin of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins, because the protein is a good, persistent film to administer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSGRGGLGGQ-----GAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQTSGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSMASGRGGLGGQGA-GAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and hair.
                                          QGTSGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAA
                                                                                                     AAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGS
                                                                                                                                                                 gagagaaagagagagggggggggagaragaaaaaagagaggaagysrggragaagagaga
                                                                                                                                                                                                           GQGAGAAAAAAAAAGGAGQGGYGG---LGSQGTSGPG-GYGPGQQTSGRGGLGGQGAGA
                                                                                                                                                                                                                                                AGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAAAGGAGQGGYG-GLGSQGTSGRGGLG
                                                                                                                                                                                                                                                                                                                                                                                   AAAAAAAAAAGGAGQGGYGGLGSQG-----TSGRGGLGGQGAGAAAAAAAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGGLGGQGAGAAAAAAAAAGGAGQGGYGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gaggygrgagagagaaagagagaggyggq-sgygagagaaaaagagaggaggy----g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQGGYG-----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gagaggyggggggagagaaaaaaagagsgggggggggagagaaagagag--agsyg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    abgagagaggagygggyg-----agagagaaaaagagagaggaggygrgagagagaaa 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAA---AGGAGQGGYGGLGSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggygrgaggygggggggagagagaaaaagagaggggggy-----grgagagaga
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                                                                                                                                                                                                                                                                                                                                                                                                                         348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $
---yagagaaagagaaagagagagy
                                                                                                                                                                                                                                                                                                                                     -gagaggygggggygagagagaaaatgaggaggygrgagagagaaagag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  í,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arraudeau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1395; DB 20
Pred. No. 9.9e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                               -ggqggygagagagaaaaa--gagsggaggygr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203;
ggqggygagagaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
579
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                                                                                                                                                                   499
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11

GSMASGRGGLGGQGAG----AAAAAAAAAAAGGAGQGGYG-GLGSQGTSGRGGLGGQGAGA 65

Matches

363;

Conservative

25;

Mismatches

DB 16; -90; 242;

Length

93;

Gaps

35;

Query Match Best Local Similarity

38.1%;

Score 1331.5; DB Pred. No. 4.7e-90;

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RESULT 1
AAR99059
AD AP99059
AD AP99059
AX AAR9
AX Spid
AX Spid
KW Fibr
CO Synt
AX (DU)
AX (DD)
CO DP-
CO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
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                                                                                                                                                                                                                                                                differ from the consensus repeat sequence by deletions of integral multiples of five consecutive amino acids consisting of the pentapeptide sequences GPGGY or GPGQQ. Synthetic analogues of DP2 were designed to mimic the repeating consensus sequence of the natural protein and the pattern of variation among individual repeats. The analogue DP-2A is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a synthetic spider dragline variant pol DP-2A. The sequence of the DP-2A monomer is given in AAR99058. DP-2A. The sequence and is rich in Gly and Ala. It is unl DP-1 except for the region of consecutive Ala residues. The representation of the protein and the pattern of variation lead to the production of the consensus sequence given in AAR99085. The ind repeats differ from the consensus sequence according to a patter
                                                          composed of tandemly repeated 119-amino acid peptide monomers which comprises three repeats which differ according to (1)-(2) above. This 119 amino acid monomer is repeated 1-16 times in the DP2 analogues. The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spider; dragline protein; variant; monomer; polymer; fibre forming region; Spidroin 1; Nephila clavipes; DP1; mimi DP-1A analogue; fibre; high tensile strength; elasticity; clo rope; surgical suture; implant; reinforcement; film; coating.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR99059 standard; Protein; 714
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DUPO) DU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640 AAAGGAGQGGYG-GLGSQGTSGPGGYGPG 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be generalised as follows:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ga--gagrggygrgagaggygggggggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dragline variant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1) the poly-alanine sequence varies in length from 6-10
                                                                                                                                                                                                                                                                                                                                                                                                                                       (2) aside from the poly-alanine sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PONT
      714 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 103-105; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US06689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEMOURS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DP-2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ဗ
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                                                                                                                                                                                                                                                                                                                                                                                                                                          individual repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP1; mimic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The repetitive
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                                                                                                                 Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscreen; hormone; moisturizer; skin disorder; skin disorder.
                                                                                                                                                                         Polymer of an analogue of spider silk protein spidroine major
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens
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                                        -GPGGY 500
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Search completed: July 3, 2001, 14:58:08 Job time: 438 sec

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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/
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61.1
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(without alignments)
283.323 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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3493
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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US-09-317-8448-2
US-09-34-177-3
US-09-34-177-3
US-08-458-298-2
US-08-478-5098-64
US-08-477-5098-64
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Sequence 2, Appli
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Sequence 2, Appli
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Sequence 31, Appli
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Sequence 33, Appli
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Sequence 36, Appli
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1 US-08-089-862-11 1 US-08-587-333-18 5 PCT-US94-07776-16 2 US-09-010-928B-4 1 US-08-687-333-13 5 PCT-US94-07776-11 1 US-08-887-333-13 5 PCT-US94-07776-11 1 US-08-477-509B-80 1 US-08-175-155-45 2 US-08-175-155-45 2 US-08-010-928B-28 1 US-08-707-237A-51 2 US-08-707-237A-51 2 US-08-175-155-53 1 US-08-477-509B-88 2 US-08-017-337A-61 3 US-08-477-39B-88 2 US-08-010-928B-2
US-08-089-862-11 US-08-587-333-18 PCT-US94-07776-16 US-09-010-928B-4 US-08-87-333-13 PCT-US94-07776-11 US-08-477-509B-80 US-08-477-509B-80 US-08-175-155-45 US-08-175-155-45 US-08-175-155-83 US-08-175-155-83 US-08-175-155-83 US-08-175-155-83 US-08-175-155-83 US-08-175-155-83 US-08-175-155-83 US-08-175-155-83 US-08-177-237A-61 US-08-477-509B-88 US-08-477-509B-88 US-08-477-958B-88

ALIGNMENTS

; TYPE: amino ac ; TOPOLOGY: line ; MOLECULE TYPE: p US-08-425-069-2 RESULT 1 US-08-425-069-2 Sequence 2, Application US/08425069 Patent No. 5728810 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: MUTPHY Jr., Gerald M REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 1447-106P TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 718 amino acids TYPE: amino acid TOPOLOGY: linear GENERAL INFORMATION: CORRESPONDENCE ADDRESS: ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5728810th Washington Street CITY: Falls Church STATE: Virginia COUNTRY: U.S.A. COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/425,069 FILING DATE: 19-APR-1995 COUNTRY: U.S.A. ZIP: 22046 COMPUTER READABLE FORM: MEDIUM TYPE: Flopy disk APPLICANT: Xu, Ming APPLICANT: Hinman, Michael B. APPLICANT: Hinman, Michael B. TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF NUMBER OF SEQUENCES: 69 APPLICANT: APPLICANT: TELEFAX: (703) 205-8050 Lewis, Randolph V. protein 2

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Query Match 61.1%; Score 2135; DB 1; Best Local Similarity 68.3%; Pred. No. 7.4e-151; Matches 495; Conservative 15; Mismatches 39;

Length 718; Indels 176;

Gaps

34;

23 QGAGAAAAAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGGQGAG-AAAAAAAAAAAAGGAGQ 79

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US-08-317-844B-2
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Patent No
                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Lewis, Randolph V.

APPLICANT: A. Ming

APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK

TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED

TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THERE

NUMBER OF SEQUENCES: 62
                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & STREET: 301 No. 5989894th Washington
 COMPUTER READABLE MEDIUM TYPE: F1
                                  STREET: 301 No. 598:
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22046
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; LENGTH: 718 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-317-844B-2
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Best Local Similarity 68.3%;
Matches 495; Conservative 1
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TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                                                                                   GGYGGLGSQGAGR---GGQGAGAAAAAVGAGQEGIRGQGAGQGGYGGLGSQG-SGRGGL
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 QGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGY
                                                      GGQGAGAAAAAAGGAGQGGLGGQGAGQGAGAAAAAAGGVRQGGYGGLGSQG----AGRGG
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38; Pred. No. 7.4e-151;
15; Mismatches 39;
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Best Local (
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Patent No. 6127146
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 747 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN FIBROUS PROTEIN
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,177
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                 LIBRARY: GenBa
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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STATE: CA
                                                                                                                                                                   23 QGAGAAAAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGGQGAG-AAAAAAAAAAAAGGAGQ
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                   Local Similarity
                         G---AAAAAAAGGAGQGGYGGLGNQG--
                                                                   GGYGGLGSQG----AGRGGQGAG----AAAAAAGGAGQGGYGGLGSQG-AGRGGLGGQGA 107
                                                                                                 GGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGA 139
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3174 Porter Drive
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ilarity 68.3%;
Conservative 1:
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                                                                                                                                                                                                                   Score 2135; DB 4;
Pred. No. 7.6e-151;
                                                                                                                                                                                                   Mismatches
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   -AGRGGQG--
                                                                                                                                                                                                                                  Length 747;
                                                                                                                                                                                                   Indels 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08209747 Patent No. 5733771 GENERAL INFORMATION:
                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,747
FILING DATE: 14-MAR-1994
CLASSIFICATION: 530
CLASSIFICATION: 530
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lewis, Rando
APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDN
TITLE OF INVENTION: Sil
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637 GGVGS 641
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STREET: P.O. Box 747
CITY: Falls Church
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acid
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FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: N. clavipes
TISSUE TYPE: minor ampullate gland
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                615 LGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYG 651
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Pred. No. 5.8e-97;
                                                                   -GGQGGYGAGAGAAAAAGA--GAGRGGYG-
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                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: N. clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNAS Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE: minor ampullate gland FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
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APPLICANT:
196 AAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAA-------AAAAAG 239
                                                                              184
                                                                                                                 136 GQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAA 195
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STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                             y Match 40.2%; Score 1405; DB 1; Length 832; Local Similarity 50.1%; Pred. No. 5.8e-97; hes 349; Conservative 17; Mismatches 207; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-104P
                                                                                                                                                                                                                                                        21 GGGGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQG
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                         amino acid
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RESULT 6
US-07-609-716-31
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Patent No. 5514581
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                                                                                                         TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
                                                                                                                                            REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ferrari, Franco A. APPLICANT: Cappello, Joseph
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      578
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                 TOPOLOGY:
                                TYPE: amino acid
STRANDEDNESS: si
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ZIP: 94111
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CITY: San Francisco
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Suite 3400
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Best Local Similarity
Matches 286; Conserv
                                                                                                                                                                               GENERAL INFORMATION:
                                     APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W.
APPLICANT: Dorman, Mary A.
TITLE OF INVENTION: Methods for Preparing Synthetic
TITLE OF INVENTION: Repetitive DNA
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186
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STREET:
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                                ADDRESSEE:
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5641648
   San Francisco
                E: Flehr, Hohbach, Test, Albritton & Herbert Four Embarcadero Center, Suite 3400
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41.0%; Pred. No. 3.5e-84;
+iva 58; Mismatches 311;
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US-08-175-155-29
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Best Local Similarity
Matches 286; Conserv
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INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETTTAM I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55186-5/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
                                                                                                        520 AAAAAAAAAGGAGQGGYGGLGSQGTSGRG---GLGGQGAGAAAAAAAAAAAAGGAGQGGYGG 576
                                                                                                                                                          512 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGA
                                                                                                                                                                                                                                                                                                                                                                                   392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 GQGAGAAAAAAAAGGAGQGGYGGLGSQGTSGRG---GLGGQGAGAAAAAAAAAAAGGAG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 29-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 MASGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLG----GQGAGAAAAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                      GAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIGGQGAGAAAAAAAAAGGAGQGGYGGIGSQGTSGPGGYGPGQQT---SGRGGIGGQG 352
LGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYG-----GLGSQGTSGRGGLGGQ 629
                                                  GSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAG
                                                                                                                                                                                                                GGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQT---SGRGGLGGQGAGA 519
                                                                                                                                                                                                                                                                                                                        YGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYG-----GLGSQGTSGRGGL 462
                                                                                                                                                                                                                                                                                                                                                                                 AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                AGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG----GLGGQGAGAAAAAAAAAAAGGAGQGG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYG-----GLGSQGTSGR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQT----SGRGGLG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGAGSGAGAGSGAGAGSGAGAGSGAAGSGAAGSGAGAGSGAGAGSGAGAGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAG-GAGQGGYGGLGSQGT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.3%; Score 1233.5; DB
41.0%; Pred. No. 3.5e-84;
ative 58; Mismatches 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/175,155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                     631
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US-08-477-509B-64
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                                                                                Matches
                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                               TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: 07-7UN-1995
CCLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/114,010
APPLICATION NUMBER: US 07/114,010
ETLING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
APPLICATION O4-NOV-1986
FTILING DATE: 04-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John w
APPLICANT: Dorman, Mary A
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the
                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION IMPORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/114,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ferrari, Franco A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                    13 MASGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLG---GQGAGAAAAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
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CITY: San Francisco
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                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Trecartin, Richard F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
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                                                                                                                                                                                                                                                                             1177 amino acids
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                        415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1993
                                                                                                                                                                                                                                      single
                                                                            35.3%; Score 1233.5; DB 1; Length 1177;
41.0%; Pred. No. 3.5e-84;
tive 58; Mismatches 311; Indels 43;
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US-08-707-237A-35
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35, Application US/08707237A Patent No. 5830713
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL
                SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/707,231 FILING DATE: 03-SEP-1996
                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Ho
                                                                                                                                                                                                                                                                                            APPLICANT: DORMAN, MARY A.
TITLE OF INVENTION: METHODS FOR PREPARING
TITLE OF INVENTION: REPETITIVE DNA
                                                                                                                                                                                                                                                                                                                                APPLICANT: Ferrari, Franco A. APPLICANT: Capello, Joseph APPLICANT: Crissman, John W. APPLICANT: Dorman, Mary A.
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                                                                                                                                                         COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                       STREET: Four Embarce
CITY: San Francisco
STATE: California
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                                                                                                                                                                           COUNTRY:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYG------GLGSQGTSGRGGL 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAG 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQT---SGRGGLGGQGAGA 519
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                                  US/08/707,237A
                                                                    Version
                                                                                                                                                                                                                                                                                                                SYNTHETIC
                                                                    #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: 4.55186-10/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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APPLICATION NUMBER:
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  463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 MGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 MASGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLG----GQGAGAAAAA 69
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TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 09-NOV-1988
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GGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQT---SGRGGLGGQGAGA 519
                                             GAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAG
                                                                                      YGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYG-----GLGSQGTSGRGGL 462
                                                                                                                                                                                                                          GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSG
                                                                                                                                                                                                                                                                GGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQT----SGRGGLGGQG
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                                                                                                                                 AGAGSGAGAGSGAGAGSGAGAGSGAAGSGAAGSGAGAGSGAGAGSGAGAGSGA 451
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                                                                                         TELEFAX: 415-398-3249 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 06/927, 258
FILING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W.
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
NUMBER OF SEQUENCES: 112
                                                                                                                      NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                          SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
                             TYPE: amino acid
STRANDEDNESS: si
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                  TOPOLOGY:
                                                             LENGTH:
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                                                           1177 amino acids
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Pollock, Thomas J.
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Chambers, James
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                  linear
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Suite 3400
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Matches
   STATE: CA
COUNTRY: US
ZIP: 94111
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RESULT 11
US-08-475-411A-31
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                                                                                                                                                                                                                 GENERAL INFORMATION:
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test,
STREET: Four Embarcadero Center,
                                                                                                                  APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                630 GAGAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPG 667
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nes 286; Conserv
STREET: Four Embarca
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 GAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAG 151
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                                                                                                                                                                                                                                                                                                                                                                                    GAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAG
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41.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1233.5; DB Pred. No. 3.5e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                        Albritton & Herbert
Suite 3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

US/08/475,411A

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FILING DATE: 06-NOV-1990
PRIOR APPLICATION UNBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/114,618
FILING DATE: 29-CCT-1987
PRIOR APPLICATION UNBER: US 06/927,258
FILING DATE: 04-NOV-1986
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
APPLICATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: 3-55186-9/RET/MTK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 286; Conserv
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INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Relea
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 07-JUN-1995
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PRIOR APPLICATION DATA:
                                      410
                                                                                                                                                                                                                                                                                                                                                                                              152
  452
                                                                                                                                                          332
                                                                                                                                                                               296 GGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQT---SGRGGLGGQG 352
                                                                                                                                                                                                                                      272
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STRANDEDNESS: sir
                                  YGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYG-----GLGSQGTSGRGGL 462
                                                                                                                                                                                                                                                                        QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYG-----GLGSQGTSGR 295
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                                                                                                                AGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG---GLGGQGAGAAAAAAAAAAAAGGAGQGG
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                                                                                                                                                                                                                                  SGAGAGSGAGAGSGAGAGSGAGAGSGAAGSGAAGSGAGAGSGAGAGSGAGAGS
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                                                                           AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.3%; Score 1233.5; DB 4; Length 1177; Illarity 41.0%; Pred. No. 3.5e-84; Conservative 58; Mismatches 311; Indels 43;
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-478-029A-31
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                                                                                                                                  REFERENCE/DOCKET NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-8/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEPAX: 415-781-1989
INFORMATION FOR SEQ ID NO: 31:
SEGUIFANT CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
APPLICATION: 04-0V-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PAPICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION NUMBER: US 07/269,429
APPLICATION NUMBER: US 07/269,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 119
                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
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CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 94111
                                                           STRANDEDNESS:
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                                                           single
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RESULT 13
US-08-175-155-48
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                                                                                                         NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESSE: Flahr, Hohbach, Test, Albritton & Herbert
ADDRESSEE: Flahr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                            APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W.
APPLICANT: Dorman, Mary A.
TITLE OF INVENTION: Methods for Preparing
TITLE OF INVENTION: Repetitive DNA
NUMBER OF SEQUENCES: 69
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 GQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG----GLGGQGAGAAAAAAAAAAAGGAG
                                    COUNTRY:
                                                           STREET: Four Embarca
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 GAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAG 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGFGGYGFGQQT---SGRGGLGGQG
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41.0%; Pred. No. 3.5e-84;
vative 58; Mismatches 311; Indels 43;
                                                                                                                                                                                                                          Synthetic
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STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-175-155-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 48
SEQUENCE CHARACTERISTICS:
LENGTH: 1059 amino acids
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COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: A-55186-5/BIR TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
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NAME: ROwland, Bertram I.
REGISTRATION NUMBER: 20015
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 GSMASGRGGIG-GQGAGAAAAAAAAAAGGAGQGGYGGIGSQGTSGRGGIGGQGAGAAAAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTS 129
                         AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAMDP
                                                                  AGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGP 666
                                                                                                                                         RGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGG
                                                                                                                                                                                                     GSGAGAGSGAGAGSGAG - - - AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
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US-08-707-237A-54

: Sequence 54, Application US/08707237A

: Patent No. 5830713
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Query Match 33. Best Local Similarity 40. Matches 270; Conservative
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/707,237A
FILING DATE: 03-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
FILING DATE: 29-DEC-1993
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INFORMATION FOR SEQ ID NO: 54:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Trecbrtin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-10/WHD
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING TATE: 06-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 06/927,258
FILING DATE: 04-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
FILING DATE: 06-NOV-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
FILING DATE: 22-APR-
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MEDIUM TYPE: Floppy disk
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FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DOTMAN, MATY A.
TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
TITLE OF INVENTION: REPETITIVE DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: unk
TOPOLOGY: unknown
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                         1059 amino acids
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Crissman, John W.
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22-APR-1993
                                                                                                                                                                                                                                                                                                                             unknown
                                          33.7%; Score 1176.5; DB 2; 40.8%; Pred. No. 5.1e-80;
    ;09
    Mismatches
    319;
    Indels
                                                                            Length 1059;
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 83, Application US/08477509B Patent No. 5770697
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                         APPLICANT: Crissman, John w
APPLICANT: Dorman, Mary A
APPLICANT: Dorman, Mary A
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding
NUMBER OF SEQUENCES: 112
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                              CITY: San Francisco
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Crissman, John w
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PatentIn Release #1.0,
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Version #1.30
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FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATE:
APPLICATION DATE: US 06/927,258
APPLICATION NUMBER: US 06/927,258
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-3989
TELEPHONE: 415-781-3989
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Best Local Similarity
Matches 270; Conserv
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INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 1101 amino acids
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APPLICATION NUMBER: US 08
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
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                                488 GLGSQGTSGPG-GYGPGQQTSGRGGLGGQCAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSG 546
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TYPE: amino acid
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Search completed: July Job time: 524 sec 3, 2001, 14:56:34 This Page Blank (uspto)

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ALIGNMENTS

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Qy 391 AGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGG 450	Qy 349 GGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQG 390	Qy 290 QGTSGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGP-GQQTSGRGGL 348 : : :	Qy 251 SQGTSGRGGLGGQGAGAAAAAAAAGGAGQGGYGGLGS 289	Qy 200 AGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLG 250	Qy 140 GAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAA 199	Qy 80 GGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGA 139	Qy 23 QGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAG-AAAAAAAAAAAAGGAGQ 79	Query Match 61.1%; Score 2135; DB 2; Length 718; Best Local Similarity 68.3%; Pred. No. 5.8e-113; Matches 495; Conservative 15; Mismatches 39; Indels 176; Gaps 34;	A; Actus: preliminary A; Molecule type: DNA A; Residues: 1-718 <xua> A; Cross-references: GB:N37137; NID:g159711; PID:g159712 A; Note: the authors translated the codon GGT for residue 292 as Gln, GTA for residue</xua>	R;XU, M.; Lewis, R.V. Proc. Natl. Acad. Sci. U.S.A. 87, 7120-7124, 1990 A;Title: Structure of a protein superfiber: spider dragline silk. A;Reference number: A36068; MUID:90384959	major ampullate fibroin protein - orb spider (Nephila clavipes) (fragment) C;Species: Nephila clavipes C;Species: Nephila clavipes C;Date: 08-Mar-1991 #sequence_revision 13-Jan-1993 #text_change 09-Sep-1997 C;Accession: A36068

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68 AAAAAAAGGAGOGGYG	GGYGF-GQCTSGRGGLGGQGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA	371 AGAVAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAAAAAAAGGAGQRGYGG 419 451 LGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGP 497
RESULT 3 F70806 F70806 hypothetical glycine-rich protein Rv3508 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: F70806 R;Cole, S.T.; Brosch, R; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987 A;Accession: F70806 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-1901 <col/> A;Cross-references: GB:AL02202; GB:AL123456; NID:93261554; PIDN:CAA17745.1; PID:9292 A;Cross-references: Strain H37Rv C;Genetics: A;Gene: Rv3508 C;Superfamily: collagen alpha 1(IV) chain	Db 878 6ĠYGWĠDĠĠYĠSDŚAĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀ	Qy 286 GLGSQGTS-GRGGLGGQGAGAAAAAAAAAGGAGQGGYG 323

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hypothetical glycine-rich protein Rv3514 -
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-J
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  Garnier,
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  T.; Churcher, C.; Harris, D.;
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; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Natture 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the compl A;Reference number: A70500; MUID:98295987
A;Accession: D70807
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         AAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAAGGA------GQGGYGGLGSQ
                                               DPGKGGTGGTG-GTGGSGGAGGSGGANFNGGTGGTG--GTGGKGGLNTDGLSSATSGTGG
                                                                                   TSGRGGLGGQGAGAAAAAAAAAAGGAG-QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAA
                                                                                                                         SCAGGTNGSGGAGGTCGQVVAGGAGISFSNGSNGGTGGTGGVG--GTGGDGGNAGTGAG
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5%; Pred. No. 1.4e-63;
36; Mismatches 267;
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TGGTGGKGGTGGAGDDSAGGTGGTGGAGGNAGAGGLANTGGTAGNAGIGGDGGQGGNGGQ

1029

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hypothetical glycine-rich protein Rv3512 - Mycobacterium tuberculosis (strain H37 c;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: B70807 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 R;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987 A;Accession: B70807 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
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A;Residues: 1-1079 <COL>
A;Cross-references: GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA17749.1;
A;Experimental source: strain H37Rv
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                        RGGLGGQG------AGAAAAAAAAAAAAGG-AGQGGYGGLGSQ--GTSGRGGLGGQGA 429
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                                                                                                                                                                                                                                 AAAAGGAG-----QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGL 325
                                                                                                                                                                                                                                                                               GGNGGAAGAATAGSNGGAGTGSAGGNG--GTGGRGGSGGAGGDGIGGVGGGKGGNGADGE 392
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QGGAGGAGGTGGNGTGGTAGTAGAAGNGGAAGKGGAGGQGGTGGGTGGQGGAGGDGG
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                                                                                                                                                                                                                                                                                                                                                                         TGGTGGNGGNGAIGGAGGDAGGSGNSGGNGGIGGKGGNAGAGGAAGSNGGTVGANGTGGD
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987

A;Accession: A70934
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C;Species: Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: A70934
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A;Restidues: 1-1306 <COL>
A;Cross-references: GB:ALO21942; GB:AL123456; NID:g3242298; PIDN:CAA17449.1; PID:g290
A;Experimental source: strain H37Rv
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                                                                                                                                                                                                                                                                               GRGGAGGLGFGSEAPGRPGGAGGTGGAGGNGGTQAGDGGTGGAGGAGGDGGSGGAGSIGF
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                                           LGGQGAGAAAAAAAAAAAAGG-AGQGGYGGLGSQ-------GTSGRGGLGGQG--
                                                                                                                                                                                                                                                                                                                           GAAAAAAAAAAAGG-----AGQGGYGGL------GSQGTSGRGGLGGQGA----
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AGGSGGAWAGNGGTGGAGGTGGVGGTGGSGSDGVNGSSAGADGHPGGTGGVGGTGGKGGD
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                                                                                            {\tt RGADATGFGQTGASGGRGGDGGLVGNGGAGGAGGNGSKGLPGLGRLGNPGLDGGTGGNGG}
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Length 1306; Indels 194;

Gaps

35;

the complete

geno

Holroyd,

Gordon

H37RV)

----GTSGRGG

685 221 625

745 264 186

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RESULT 7

270806

E70806

hypothetical glycine-rich protein Rv3507 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 .

C;Accession: E70806

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skeiton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987

A;Accession: E70806

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-1381 <COL>
A;Cross-references: GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA17744.1; PID:g292444
A;Experimental source: strain H37RV

C;Genotics.
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A:Gene: Rv3507
C:Superfamily: collagen alpha 1(IV) chain
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 GLGGAGGMGGTGGGTGGNGGNGALLIGAGGVGGAGGIGGQGTGAGGAAGAGGTG--G
                    GAGAAAAAAAAAAAGGAGQGGYGG-----LGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAGGAG
                                                                                            GRGGLGGQGAGAAAAAAAAAGG-----AGQGGYGGLGSQ-----GTSGRGG-----LGGQ 61
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                                                                                                                                      33.9%; Score 1182.5; DB 2; ilarity 38.8%; Pred. No. 1.4e-59; Conservative 32; Mismatches 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1229
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                                                                                                                                          Indels 199;
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D Qy	117 281	QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGP 169
V	170	GGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAAAAAAAAGAGGGGY 208
В	339	GHGGAGGMGGGGTGGMGGAGGDGTTVIAAGTGGEGGTGGAAGAGGAAGARGALTSGGLA 398
Qy	209	GGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGT 254
В	399	GGVGAGGTGGTGGTGGNGADAAAVVGFGANGDPGFAGGKGGNGGTGGAAVTGGVAGDGGT 458
Qy	255	SGRGGLGGQ
Db	459	GERGGTGGAGGAGNDAGSTGNPGGRGGDGGIGGAGGAGGAGTGNGGHAGNTGDGGDGGT 518
Qy	288	GRGGLGGQGAGAAAAAAA
₽b	519	GGNGGNGTGGVNGADNTLNPDTPGGAGEPGGAGGAGGAGGAAGGPGGTGGTGGNGGNG 576
δĀ	332	GPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTS 381
. d d	577	GNGGNGGNGGNGGNAGNNSTNAPVGGEG-GAGGDGGAGGAANGGTAGSQGTG 633
Qγ	382	GRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAA 437
В	634	D
Оу	438	AAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAA 479
В	684	GGTGGSGGNGGDGGAGGNGIPGTGTEPAGGTGAKGGDGGDGGAGGAGGNAGGAG 743
VΩ	480	GAGQGGYGGLGSQ
Вb	744	GOGGNAGOGGAGGNAVIPGDGVGKAPHGDAGGSGGDGGKG-GQGGSGGTGGSGAP 800
ОУ	518	-GAAAAAAAAAAAGGAGQGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQG 572
В	801	IGGGAGGTGGSGGHAGKGGAGGTGAQGTTITVPGNGGNAGDGGNGGNAGAGGNGGSG 857
Qy	573	GYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAGGAG-QGGYGGLGSQGTSGRGGLGGQGA 631
B	858	DFGGNTTSGASGSGGNGG-NAGTAGSGGAGGTGGTGLSGGNGGNGGNGGNGGDGGNGA 914
Оу	632	-GAAAAAAAAAAGGAGQGGYGGLGSQ-GTSGPGGYGPGQQTSG 672
ф	915	HGTVGAQEVPATSLPTPNGGAGGNGGTGSNGGAPGPAG-APGPTTGG 960
A70869 hypoth C;Spec C;Date	etic ies:	A70869 A7
R;Cole ; Conr Rajand	Cole, S.T. Connor, R. jandream,	R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A; Authors: A; Title: D A; Reference	e: I	Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. Deciphering the biology of Mycobacterium tuberculosis from the complete geno ce number: A70500; MUID:98295987
A; Stat A; Mole	cule	ACCESSION: A/0809 Status: preliminary; nucleic acid sequence not shown; translation not shown Molecule type: DNA
A; Resi A; Cros A; Expe	.dues erime	RESIGNES: 1-1660 <col/> Cross-references: GB:ALO21246; GB:AL123456; NID:g3261507; PIDN:CAA16067.1; PID:g279 Experimental source: strain H37Rv
C; Genet A; Gene:	Genetics: Gene: Rv2	CS:

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                                                                                                                                                                                                                        LFGDGGAGGDGADGTAAEALGGDGGAGGAGGKGGDAGDIGDGGDGGKGGDGAHGALGGLT 127
                                                                                                                                                                                                                                          TSGRGGLGGQGAGAAAAAAAAAAAGGA-GQGGYGG----LGSQGTSGRGGLGGQGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAAGGAGQGGYGGLGSQGTSGR------GGLGGQGAGAAAAAAAAAAAAAAAAAAGGAGQGGY 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGGQGAGAAAAAAAAAAGGAGQ------GGYGGLGSQG-TSGRGGLGGQ-GAGAAAAA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G--AGAAAAAAAAGGAGQGGYGGL-GSQGTSGPGGYG------PGQQTSGRGG
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                                                                                                                           AGQGGYGGLGSQGTSGPGGYGPGQQTSG 672
                                                                                                                                                             VAGGNGGAGGAGGAGGAFLGDGGNGGAGGQGGAGRGGSPGGGGGGGGGGGAGGDAGM
                                                                                                                                                                                                                                                                                      GRGGLGGDSGNGTSAANGVDASKHGPLTGGDGGVGGNGAKAAAAGGDGGQGGDG--GNAG
                                                                                                                                                                                                                                                                                                                   GRGGLGGQ-----
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                                                                                                                                                                                                                                                                                                                                                                                 GG----LGSQGTSGPGGYG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGNGGDGAAGANGANSGAPGSDALALGQPGGNGGQGDAGQAGGAGGAGGAGGSVSG
                                                                                                                                                                                         -----GAAAAAAAAAGGA--GQGGYGGLGSQGTSGRGGLGGQGAGAAA-AAAAAAAGG 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                   H37RV)
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gc; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: H70846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-1538 <COL>
A;Cross-references: GB:ALO21841; GB:AL123456;
A;Experimental source: strain H37Rv
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C;Superfamily: collagen alpha 1(IV)
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Best Local Similarity
Matches 317; Conserv
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                                                                          GYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAAGG------AG
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                                                                                                                                                       AAAAGG-----AGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQG 484
                                                                                                                                                                                         GQGAGAAAAAAAAAGGA----GQGGYGGLGSQG-----TSGRGGLGGQGAGAAAAAA 436
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                                        GKGGNGGDG--GNYGLGGDAGSGGAGGNGGIGTDAGGAGGAGGAGGNGGSSKSTTTGNAG 1254
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Pred. No. 4e-58;
Prematches 308;
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	Db 496 NGLGAGADGTDGGRGGNGGAGGGGGAGGQGGKALAATHQDGSMGAGGAGGNGGAGGMGGD 555 Qy 323 GGLGSQGTSGPGGYGPGQQTSGRGGLGGQGA353
	296 GGLGGGGAGAAAAAAAAAAAAAAAAAAAAAAA
	Qy 251 SQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGA-GQGGYGGLGSQGTSGR 295
	Qy 201 GGAGOGGYGGLGSQGTS-GRGGLGGQGAGAAAAAAAAAAGGAGQGYGGLG 250
	Qy 151 GGAGGGGYGGLGSGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAA 200
	Qy 106 AAAAAAAGG-AGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAA 150
	Qy 46 GLGSOGTSGRGGLGGOGAGAAAAAAAAAAAAGGAGQGGYGGLGSOGTSGRGGLGGOGAGAAA 105
	Qy 11 GSMASGRGGLGGQGAGAAAAAAAAAAGGAGQGGYG 45
35;	Query Match 32.8%; Score 1145; DB 2; Length 1329; Best Local Similarity 35.9%; Pred. No. 1.7e-57; Matches 323; Conservative 35; Mismatches 300; Indels 242; Gaps 3
PID:g2131046	A;Residues: 1-1329 CCOL> A;Cross-references: GB:Z95844; GB:AL123456; NID:g3250713; PIDN:CAB09271.1; PID A;Experimental source: strain H37Rv C;Genetics: A;Gene: Rv1450c A;Gene: Rv1450c C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal
	A;Accession: E70917 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
ete genome	A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987
D.; Gordon, S l.; Holroyd, S. , S.	Churcher, C.; Harris, Gentles, S.; Hamlin, N ; Skelton, S.; Squares
	xt_change 20-Jun-20
n H37RV)	RESULT 10 E70917 hypothetical glycine-rich protein Ryl450c - Mycobacterium tuberculosis (strain
	Db 1435 NGCAGAGGGSLSTGQSGGPRR 1455
	Qy 661 PGGYGPGQQTSGIRR 675
···· <u>,</u> ,	Qy 636 GAAAAAAAGG AGGGGYGGLGSQGTS 660
	Db 1315 GGNGSSGAASGSGVVNVTAGHGGNGGNGGNGGNGSAGAGGGGGGGGGGGGGGGGGGGG
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630 GAGAAAAAAAAGGAGQGGYGG-LGSQGTSGPGGYGPGQQTSGIRRPAAKL	Qγ
910 LGGFGGNGAAGANGVAVGAPGQPGGAGGHGGAGGNGGAGGNGGQGVVSDGAGGAGGAGGA	Db
588 LGGQCAGAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQ	Qγ
851 GTGGNGGRGGDGAFGGNSANATNPGENGPNGNPGGNGGAGGAGGAGLNG-GNGGAGGNGG	몽
543 GTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGG	Qy
796 QGGSGGAGSTPGAKGAHGFTPTSGGDGGDGGNGGNSQVVGGNGGDGGNGGNGGSA	밁
492 QGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGL-GSQ	Qy
736 GGLAGNLFGQNGIQGVGGSGGKGGAGGLAGDGGNGANGNFAFGDGNGGHGGNGGNPGAGG	밁
449 GGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGGGYGGLGS	Qy
676 AGGAGGAGGRGGDFGGDGGTGGAGGNGANGANATTPGAKGGDGGHGGPGAQGGNGGQGGP	Db
GSQGTS	Qy
616 GNGANATVAGGAGGKGGNGGLVGNGGAGGKGGDGMAGVAGSSPTTAGESGTSGQNGG	망
354GAAAAAAAAAAGGAGGGGGGGGGGGGGGGGGGGGGG	Qy
:: 556 GGNGAKGTFDNGGDGVGGNGGSNGGSRGIGGAGGTGGAGSTAGADGARGATPTSGGNGGTG	밁

ULT 1

hypothetical glycine-rich protein Rv1091 - Mycobacterium tuberculosis (strain H37RV) C; Species: Mycobacterium tuberculosis C; Date: 17.Jul-1998 #sequence_revision 17.Jul-1998 #text_change 24.Nov-1999 C; Accession: A70896 R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 Rature 393, 537-544, 1998 Rature 393, 537-544, 1998 Rature 393, 537-544, 1998 Rature 393, 537-544, 1998 Reference number: A70500; MUD: Paylor, K.; Whitehead, S.; Barrell, B.G. A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Reference number: A70500; MUD: 98295987 R; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Accession: A70896 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Rocesule type: DNA A; Residues: 1-853 <COL> A; Cross - references: GB: AL021897; GB: AL123456; NID: 93256022; PIDN: CAA17207.1; PID: e125 A; Experimental source: strain H37Rv C; Genetics: Rv1091 C; Superfamily: unassigned collagens

Ş В Ş В Qy В Query Match 32.6%; Score 1139; DB 2; Length 853; Best Local Similarity 40.3%; Pred. No. 2.6e-57; Matches 298; Conservative 27; Mismatches 304; Indels 11 137 160 GLG--SQGTSGPGGYGPGQQTS----GRGGLGGQGA----GAAAAAAAAAAAAGGAGQGGYG 209 257 LFGDAGAGGNGGKGGAGGAAFSINFTAGDGGAGGAGGSGGHALLWGAGGAGGNGGSGGTG 316 11 GSMASGRGGLGGQGAGAAAA----AAAAAAGGAGQGGYGGLGSQGTS-----GRGGL 58 59 GGQGAGAAAAAAAAGGA------GQGGYGGLGSQGTSG----RGGLGGQGAGAAAAA 107 AAAAAGGAGOGGYGGLG------SQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYG 159 GGAGGTSVIPGVAGGNGGAGGSAGLWGTGGAGGDGGNGRSGPVNVAGSAGGNGGAGGAAG 256 GGLLYGNGGNGGTSTTAGVAGGNGGAAGLIGNGGAGGGGGGGAGAAGGNGGAGGWLYGNGGA 196 Indels 110; Gaps 28;

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spidroin 2, dragline silk fibroin - orb spider (Nephila clavipes) (fragment) % Alternate names: silk fibroin, dragline C; Species: Nephila clavipes C; Species: Nephila clavipes C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Mar-1998 C; Accession: A44112; S27824
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A;Note: sequence extracted from NCBI backbone (NCBIP:113893)
R;Hinman, M.B.; Lewis, R.V.
submitted to the EMBL Data Library, May 1992
A;Description: Isolation of a clone encoding a second dragline silk fibroin: Nephila
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J. Biol. Chem. 267, 19320-19324, 1992
A;Title: Isolation of a clone encoding a second A;Reference number: A44112; MUID:92406876
A;Accession: A44112
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A; Residues: 19-627 <HI2>
                                                                                                                                                                                                          A; Description: Isolation o
A; Reference number: S27824
A; Accession: S27824
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A; Residues: 1-627 <HIN>
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                                                     Query Match
Best Local Similarity
Matches 324; Conserv
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GGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAG----
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                                                           Conservative
                                                                         32.5%;
                                                         32;
                                                       Score 1135; DB 2;
Pred. No. 3.5e-57;
32; Mismatches 180
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                                                           180;
                                                                                             Length
                                                           Indels 146;
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987
A;Accession: A70812
                                                                                                                                                                                                                                                                                                RESULT 13
A70812
hypothetical glycine-rich protein Rv0833 - Mycobacterium tuberculosis (strain hypothetical glycine-rich protein Rv0833 - Mycobacterium tuberculosis (species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis (species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: A70812
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A; Gene: Rv0833
C; Superfamily:
                                   A; Experimental source: C; Genetics:
                                                                                          A; Molecule type: DNA
A; Residues: 1-749 <COL>
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                                                                          A; Cross-references: GB: AL022004;
                                                                                                                           A; Status: preliminary; nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --AGPGGYGP-AQQGPSGPG------PAQQGP
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                                                          strain
                                                       04; GB:AL123456; NID:g3261550;
H37RV
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                                                                                                                                 not shown;
                                                                                                                                   translation
                                                                              PIDN:CAA17639.1;
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                                                                              PID:g291
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Query Match Best Local Similarity

31.9%;

Score 1114.5; DB 2; Pred. No. 5.6e-56;

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RESULT 14
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H70987
H70987
hypothetical glycine-rich protein Rv1759c - Mycobacterium tuberculosis (strain H37R hypothetical glycine-rich protein Rv1759c - Mycobacterium tuberculosis (strain H37R hypothetical pames: wag22 antigen homolog
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Cotes: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 20-Jun-2000.
C;Accession: H70987
C;Cole. S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gord
C;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroy
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Hile: Deciphering the biology of Mycobacterium tuberculosis from the complete ge
A;Reference number: A70500; MUID:98295987
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-914 <COL>
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A;Cross-references: GB:Z95890; GB:AL123456;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv1759c; wag22
C;Superfamily: elastin
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                                                                                    ----AGAAAAAAAAAAAGGAGQGGYGG-LGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQ
                                                                                                                    SGGAGGSGGSSLSGKAGAGGAGGSAGLFYGSGGAGGNGGYSLNGTGGDGGTGGAGQITGL
                                                                                                                                                                             GTGGPGGNGGSTGAGGTGGAGGPG-GLYGAGGSGGAGGHGGMAGGGGGVGGNAGSLTLNA
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                                                          RSGFGGAGGAGGASDTGAGGNGGAGGKAGLYGNGGDGGAGGDGATSGKGGAGGNAVVIGN
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RESULT 15
B70812
hypothetical glycine-rich protein Rv0834c C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Ju

17-Jul-1998

#text_change

20-Jun-2000

Mycobacterium tuberculosis (strain

H37RV)

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C;Genetics:
A;Gene: Rv0834c
C;Superfamily: elastin
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987
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Search completed: July 3, 2001, 14:59:32 Job time: 357 sec

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Y278_MYCTU
Y278_MYCTU
YD25_MYCTU
ELS_BOVIN
EBN1_EBV
ELS_CHICK
ELS_HUMAN
Y118_MYCTU
VNUA_PRVKA
YP91_MYCTU
VNUA_PRVCTU
GRP1_PETHY
LORI_MOUSE
CAFE_RIFPA
GRP_ARATH
Y140_MYCTU
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Pred. No. 5.6e
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                            -AAAAAAGGAGQGGYGGLGSQGTSGRGGLGG
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AMEDLINE-98255987; PubMed-9634230;

AMEDLINE-98255987; Parkhill J., Garnier T., Churcher C., Harris D.,

AMEDLINE-98255987; Parkhill J., Garnier T., Churcher C., Harris D.,

AMEDLINE-98255987; Parkhill J., Garnier T., Connor R.,

AMEDLINE-98255987; Parkhill T., Garnier T., Connor R.,

AMEDLINE-98255987; Parkhill T., Garnier T., Churcher C., Harris D.,

AMEDLINE-98255987; Parkhill T., Garnier T., Churcher C., Harris D.,

AMEDLINE-98255987; Parkhill T., Garnier T., Churcher C., Harris D.,

AMEDLINE-98255987; PubMed-963428.

AMEDLINE-98255987; Parkhill T., Garnier T., Churcher C., Harris D.,

AMEDLINE-98255987; PubMed-963428.

AMEDLINE-98255987; Parkhill T., Garnier T., Churcher C., Harris D.,

AMEDLINE-9825987; Parkhill T., Garnier T., Churcher C., Harris D.,

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AMEDLINE-9825987; Parkhill T., Garnier T., Churcher T., Churcher T., Churcher T., Churcher T., Churcher T., Churcher 
                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000084; Pfam; PF00934; PE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL022022; CAA17745.1; HSSP; P19972; 1KVD. TubercuList; Rv3508; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=H37RV;
MEDLINE=98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PE-PORS FAMILY PROTEIN RV3508 PRECURSOR
RV3508 OR MTV023.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   053553;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales;
NCBI_TaxID=1773;
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hes 351;
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                                                                      GKGGVGGVAGLGGAGGAAGQLFSAGGAAGAVGVGGTGGQGGAGGAGAAGADAPASTGLTG 411
                                                                                                               GRGGLGG----QGAGAAA------AAAAAAAGG-AGQGGYGGLGSQG-------
                                                                                                                                                                                                        GSMASGRGGLGGQ-GAGAAAAAAAAAAAGGAGQGGYGGLGSQ-----
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  -TSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGR----
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                                                                                                                                                                                                                                                        Conservative
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1901
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                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                     Score 1277.5; I
Pred. No. 3.3e-5
28; Mismatches 2
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HYPOTHETICAL |
RV3508.
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Harris
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P05790; Q26379; Q17220;
Q1-NOV-1988 (Rel. 09, Created)
Q1-OCT-2000 (Rel. 40, Last sequence up
Q1-OCT-2000 (Rel. 40, Last annotation
  Nucleic [2]
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                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glo: Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOMMO
                       Zhou C.-2., Confalonieri F., Medina N., Zi
Yang T., Jacquet M., Janin J., Duguet M.,
"Fine organization of Bombyx mori fibroin
Nucleic Acids Res. 28:2413-2419(2000).
                                                                                                                                                                                                                                                                                                                                                        FIBROIN HEAVY CHAIN
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                                                                                                                                                                                                                                                                                                        Bombyx mori (Silk moth).
                                                                                                                           MEDLINE-20330362; PubMed-10871375.
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCBI_TaxID=7091;
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PARTIAL SEQUENCE FROM N.A.
MEDLINE=94365842; PubMed=7916056;
Mita K., Ichimura S., James T.C.;
"Highly repetitive structure and agene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanaka K., Kajiyama N., Ishikura K., Waga S., Kikucni A. Takagi T., Mizuno S.;
"Determination of the site of disulfide linkage between
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Cell 16:425-436(1979).
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MEDLINE-80045039; PubMed-498286;
Tsujinoto Y., Suzuki Y.;
"The DNA sequence of Bombyx mori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        light chains of silk fibroin produced by Biochim. Biophys. Acta 1432:92–103(1999)
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SECTION OF SILK GLANDS.

DOMAIN: COMPOSED OF ANTIPARALLEL BETA SHEETS. THE STRANDS OF THE DOMAIN: COMPOSED OF ANTIPARALLEL TO THE FIBER AXIS. LONG STRETCHES OF SILK FIBROIN ARE COMPOSED OF MICROCRYSTALLINE ARRAYS OF (-GLY-SER-GLY-ALA-GLY-ALA-)N INTERRUPTED BY REGIONS CONTAINING BULKIER RESIDUES. THE FIBER IS COMPOSED OF MICROCRYSTALLINE ARRAYS ALTERNATING WITH
                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: FORMS THE SILK FILAMENT; A STRONG, INEXTENSIBLE, INSOLUBLE AND CHEMICALLY INERT FIBRE.
SUBUNIT: FORMED OF TWO CHAINS: HEAVY AND LIGHT, THAT ARE LINKE A DISULFIDE BOND. HEAVY-LIGHT CHAIN ASSEMBLY IS ESSENTIAL FOR EFFICIENT INTRACELLULAR TRANSPORT AND SECRETION OF FIBROIN.
TISSUE SPECIFICITY: PRODUCED EXCLUSIVELY IN THE POSTERIOR (PSG
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EMBL; V00094; CAA23432.1; -EMBL; V00097; CAA23433.1; -EMBL; S74439; AAB3186.1; -EMBL; X13869; CAA32076.1; -EMBL; M35378; AAA27839.1; -EMBL; AB017362; BAA33147.1; --Silk; This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ SIGNAL DISULFID DOMAIN PIR; S01844; S01844. send an email to license@isb-sib.ch). Signal; Repeat AF226688; AAF76983.1; -. 21 5263 5206 5244 FIBROIN HEAVY CHAIN. HIGHLY REPETITIVE. INTERCHAIN (WITH LIGHT CHAIN)

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RESULT 4
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                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hinman M.B., Lewis R.V.;

"Isolation of a clone encoding a second dragline silk fibroin.

Nephila clavipes dragline silk is a two-protein fiber.";

J. Biol. Chem. 267:19320-19324 (1992).

-I- FUNCTION: THIS SPIDER MAJOR AMPULLATE SILK POSSESSES UNIQUE CHARACTERISTICS OF STRENGTH AND ELASTICITY. IT MAY CONSIST CHARACTERISTICS OF STRENGTH AND ELASTICITY TOWN ACCEPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                  REPEAT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
Nephila clavipes (Orb spider).
Eukaryota, Metazoa, Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                 186
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                                                                                                                                                                                                                                                      21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSEUDOCRISTALLINE REGIONS OF ANTIPARALLEL WITH ELASTIC AMORPHOUS SEGMENTS. SUBUNIT: MAJOR SUBUNIT: WITH SPIDROIN 1, CSUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                    AGQGGYGGIG-SQGTSGRGGIGGQGAGAAAAAAAAAGGAGQGGYGGIGSQ----GTSGR 131
                                                                                                                                                                                                                                                    GGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAG----G
QGPGGYG----PGQQGPGGYGPGQQGLSGPGSAAAAAAAAGPGQQGPGGYGP-GQQGPSGP
                          AGQGGYGGLGSQGTSGRGGLG-GQ----GAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGR 295
                                                                                                                                       GGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLG-----
                                                                                                                                                                                                                          GGYGPGQ------QGPGGYGP-GQQGPSGPG-----SAAAAAAAAAAAGPGGYG
                                                                                                             GQQGPSGPGSAAAASAASAESGQQGPGGYG-PGQQGPGGYGPGQQ--GPGGYGPGQQGP
                                                                                                                                                                   PGQQGPGGYGPGQQGPGRYGPGQQGPSGPGSAAAAAA-GSGQQGPGGYGPRQQGPGGYGQ
                                                     SGPGSAAAAAAASGPGQQGPGGYGP-GQQGPGGYGPGQQGPSGPGSAAAAAAAAASGPGQ
                                                                                -GQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRG----GLGGQGAGAAAAAAAAAAAAGG
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                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                Score 1135; DB 1;
Pred. No. 3.1e-44;
32; Mismatches 180;
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                                                                                                                                                                                                                                                                                                                                                     CB9B63779B2C594B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPROXIMATE TANDEM REPEATS
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Nephila.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.
Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WA22_MYCTU STANDARD; PRT; 9
006794;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
WAG22 ANTIGEN PRECURSOR.
WAG22 OR RY1759C OR MTCY28.25C.
                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
NCBI_TaxID=1773;
                                                       EMBL; 295890; CAB09322.1; HSSP; P41140; 2SFA.
                                                                                                                                                                                                                                                                                                                                                                                                                complete genome sequence. ";
Nature 393:537-544(1998).
-!- SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                  Rv1759c; -.
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CHAIN
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Antigen; Repeat;
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                                                                                                                                                  RSGFGGAGGASDTGAGGNGGAGGKAGLYGNGGDGGAGGDGATSGKGGAGGNAVVIGN
                                                                                                                                                                           ----AGAAAAAAAAAAAGGAGQGGYGG-LGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQ
                                                                                                                                                                                                       SGGAGGSGGSSLSGKAGAGGAGGSAGLFYGSGGAGGNGGYSLNGTGGDGGTGGAGQITGL
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Best Local
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Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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30-MAY-2000
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SEQUENCE 7
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                                                                          GSQGTSGR-GGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQTSGRG
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                                                                                                                                                   GAGQG-----GYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAG----
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PE-PGRS FAMILY PROTEIN RV2634C.
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                                       -GLGESLDGNDGTGGKGGAG---GTAGTDG-GAG----GAG
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RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gardon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., RA Gordon S.V., Basham D., Brown D., Chillingworth T., Connor R., RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., RA Hornsby T., Jagels K., Krogh A., McLean M.A., Rogers J., Ra Hornsby T., Jagels K., Skelton S., Squares M.A., Rogers J., Ra Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E. RA Taylor K., Whitehead S., Barrell B.G.;

TDeciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

RI Nature 393:537-544(1998).

TO -1 SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY; PGRS
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956877;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence upds
30-MAY-2000 (Rel. 39, Last annotation upds)
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RVO.278C OR MTV035.06C.
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                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Segger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TubercuList; Rv0747;
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                     351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 GQGAGAAAAAAA------AAAGGAGQGGYGGLGSQGTSGRGGLGGQ--GAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBFAMILY.
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QGA------GAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAG
                                                      GTI--GGVNG-GAGGAGGAGGILFGTGGTGGSGGPGATGLGGIGGAGGAALLFGSGGAGG
                                                                                    GTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGG
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                                                                                                                                                                                                                                                                                         GPGQQTSGRGGLGGQGAGAAAAAAAAAAGGAG-----QGGYGG----LGSQGTSG
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                                                                                                                                                                                        NGGASTGGGDGGPGGAGGTGVLIGNGGNGGSGGTGA--TLGKAGIGGTGGVLLGLDGFTA
                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAAAAGGAGQGGYGGL-GSQGTSG-----RGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYG
                                                                                                                      PASTSPLHTLQQDVINMVNDPFQTLTGRPLIGNGANGTPGTGADGGAGGWLFGNGGNGGQ
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Pred. No. 9.8e-38;
3; Mismatches 289
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POTENTIAL.
HYPOTHETICAL PE-PGRS FAMILY
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Query Match
Best Local Similarity
Matches 323; Conserv
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                                                                         CHAIN
SEQUENCE
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
ELASTIN PRECURSOR (TROPOELASTIN).
                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELN.
                                                                                                                                   EMBL; U08210; AAA80155.1; -. HSSP; P04002; IWFA. MGD; MGI:95317; Eln.
                                                                                                                                                                                                                                                                                                                                                                 Genomics 23:125-131(1994).

11- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETE:
-1- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95130069; PubMed-7829060;
Wydner K.S., Sechler J.L., Boy'd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin
mouse chromosome 5 in a region of linkage conservation with
                                                                                                       SIGNAL
                                                                                                            Structural protein; Repeat; SIGNAL 1 27
                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome 7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/C; TISSUE-Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF EI
PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
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71955
               27.9%;
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   36;
                                                                                                         Signal; Connective tissue POTENTIAL.
               Score 976; DB 1; Pred. No. 3.4e-37;
                                                                         ELASTIN.
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                                                           GFGLSPIYPGGGAGGLGVGGKPPKPYGGALGALGYQGGGCFG
                                                                         GAGAAAAAAAAAAGGAGQGG-----YGG-LGSQGTSGPGGYG
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ELS_RAT STANDARD; PRT; 864 AA.

ID ELS_RAT STANDARD; PRT; 864 AA.

Q99372;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-2000 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ELASTIN PRECURSOR (TROPOELASTIN) (FRAGMENT).

GN ELN.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat

OX NCBL_TaxID-10116;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE-91104868; PubMed-1702999;
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Rattus.

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SPILOING.";

Genomics 12:651-658(1992).

-I- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS A NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER NUCHAL LIGAMENT, ELASTIN CHAINS ARE CROSS-LINKED

-I- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED

-I- SUBUNIT: THE THE POLYMERIC BLASTIN CHAINS ARE CROSS-LINKED
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Pierce R.A., Alatawi A., Deak S.B., Boy
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Biochemistry 29:9677-9683(1990).
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ARE PRODUCED BY ALTERNATIVE SPLICING.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eigimeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                       YD25_MYCTU STANDARD; PRT; 603 AA. Q10637; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV1325C PRV1325C OR MTCY130.10C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGLG-SQGTSGR
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PGGYGPGQQTSGI
                                                                  --AGMVGNGGDGGAGGASVVANGGVGGSGGN-----ATLIGNGGNGGNGGVGSAPGKGG
                                                                                                          AAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGS-QGTSG
                                                                                                                                                                                                  QGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAA
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                                                                                                                                                                                                                                                                                               GQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGS
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Pred. No. 1.4e-32;
5; Mismatches 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 603;
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01-JUL-1989 (Rel. 11, C
01-JUL-1989 (Rel. 11, I
01-OCT-1994 (Rel. 30, I
                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phaseolus vulgaris (Kidney bean) (French bean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1989 (Rel. 11, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).
                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P30129; 4DPV. Cell wall; Structural protein; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fabales; Fabaceae; Papilionoideae; Phaseolus.
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                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHEET CONFIGURATION.
SIMILARITY: THE N-TERMINAL SIGNAL SEQUENCE OF ABOUT 30 AA SHOWS ABOUT 60% HOMOLOGY TO THAT OF THE GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN GRP 1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                S01820; S01820.
                                                                                              AAAAAGGAGQGGYGGLGSQGTSGPGGYGP-GQQTSGRGGLGGQGAGAAAAAAAAAAAAAAAAGGAG
                                                                                                                                                  GSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAA 145
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 AGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGG
                                                   QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQG
                                                                              GVAYGGGGERGGYG--GGQGGGAGGGYGAGGEHGIGYGGGGGSGAG
                                                                                                                                   G--GYAGEHGVVGYGGGS-----
                                                                                                                                                                                      GVCSARRALLTLDAGYGLGHGTG------GGYGG-----AAGSYGGGGGGGGGGGG
                                                                                                                                                                                                              GAAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGL 85
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                     33
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36683
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                                                                                                                                                                                                                                        Score 853.5;
Pred. No. 5.6e
16; Mismatches
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8 X 22 AA
                                                                                                                                                                                                                                                                                                                                                GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8.
                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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B5C4A9B983B43607 CRC64;
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Rosenbloom J.C., Abrams W.R., Indik Z
Rosenbloom J.;
"Structure of the bovine elastin gene
"Structure splicing of elastin mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELS_BOVIN STANDARD; PRT; P04985; P04986; P04997; Q29421; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence up 30-MAY-2000 (Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                  MEDLINE-91234332; PubMed-2031719;
Manohar A., Shi W., Anwar R.A.;
"Partial characterization of bovine elastin gene for human elastin.";
                                                                                                                                                                                Blochem.
                                                                                                                                                                                                                                                                                                                                                                Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Nuchal ligament;
MEDLINE-89274159; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Primary structures of bovine elastin
sequences of cDNA clones.";
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Chem. Cell Biol. 69:185-192(1991).

CHEM. CEUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY. SUBJUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER INTO AN EXTENSIBLE 3D NETWORK.

SUBGCHLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS. ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE PRODUCED BY ALTERNATIVE SPLICING.
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N., Ornstein-Goldstein N., Bashir M.M.,
Abrams W.R., Indik Z., Yoon K., Parks W.,
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EMBL; K03506; AAA30506.1; -
EMBL; W03506; AAA30706.1; -
EMBL; J02855; AAA30776.1; -
EMBL; M58652; AAA03519.1; -
PIR; A26728; A26728.
PIR; B26728; C26728.
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P03211;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-84270667; PubMed-6087149;

Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Fa
Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C.,

Tuffnell P.S., Barrell B.G.;

"DNA sequence and expression of the B95-8 Epstein-Barr
                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-DEC-1998 (Rel.
                     Petti L., Sample C., Kieff E.; "Subnuclear localization and phosphorylation latent infection nuclear proteins."; Virology 176:563-574(1990).
                                                                                                                     "Sample J., Hummel M., Braun D., Birkenbach M., Kieff E.;
"Nucleotide sequences of mRNAs encoding Epstein-Barr virus
proteins: a probable transcriptional initiation site.";
Proc. Natl. Acad. Sci. U.S.A. 83:5096-5100(1986).
                                                                                             SUBCELLULAR LOCATION
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-i- FUNCTION: INVOLVED IN LAT
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EMBL; M13941; AAA45889.1;
PIR; A03773; QQBE31.
PIR; S33021; S33021.
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01-AUG-1988
01-OCT-1996
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-I- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS A NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED INTO AN EXTENSIBLE 3D NETWORK.

-I- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FOR ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO FORMS OF CRASTIN THAT ARE PRODUCED BY ALTERNATIVE SPLICING.
-I- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
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MEDLINE-88309083; PubMed-2841924;
Baule V.J., Foster J.A.;
"Multiple chick tropoelastin mRNAs.";
"inchem Binobvs. Res. Commun. 154:1054-1060(1988).
                                                                                                                                   PIR;
                                                                                                                                                                      EMBL; M18633; AAA48761.1; -. EMBL; M21880; AAA49082.1; -. EMBL; M15889; AAA49108.1; -.
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE-87397534; PubMed-3502711;
Tokimitsu I., Tajima S., Nishikawa T., Tajima "Sequence analysis of elastin cDNA from chick tissue-specific transcription of the elastin g
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MEDLINE-87242320; PubMed-3593675;
Bressan G.M., Argos P., Stanley K.K.;
"Repeating structure of chick tropoelastin
DNA cloning.";
                                                                                        Structural
                                                                                                      PIR; A27264; A27264.
PIR; A26601; A26601.
HSSP; P04002; 1WFA.
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CURSOR (TROPOELASTIN) (FRAGMENT).
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OXIDATIVE DEAMINATION (POTENTIAL).

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22.9	22.9	23.0	23.1	23.4	23.9	24.0	24.2	24.5	25.6	25.7	25.9	26.2	26.4	26.4	27.2	27.7	27.9	28.2	28.2	28.7	28.9	29.0	29.3	29.7	30.8
606	591	639	618	584	576	902	922	610	484	904	694	626	667	923	1729	1011	810	741	714	731	636	783	837	767	882
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Best Local Similarity
Matches 457; Conserv
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046172;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DRAGLINE SILK PROTEIN SPIDROIN 1 (FRACMENT).
Nephila claripes (Orb spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Beckwitt R., Arcidiacono S., Stote R.;

Insect Biochem. Mol. Biol. 0:0-0(1998).

EMBL; U37520; AAC04504.1; -.

NON_TER 1 1 1

NON_TER 617 617

SEQUENCE 617 AA; 49410 MW; 1EF0CE92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence conservation in the C-terminal region of spider silk proteins (Spidroin) from Nephila clavipes (Tetragnathidae) and bicentenarius (Araneidae).";
J. Biol. Chem. 269:6661-6663(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-94165058; PubMed-8120021;
Beckwitt R., Arcidiacono S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6915;
63
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                                                                                                                                                                                   11 GSMASGRGGLGGQGA---GAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAA
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                                   AAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQG 127
AAAAAAAGGVGQ----
                                                                                                                                               GAGQGGYGGLGSQGAGRGGQGAGAAAAAAGGAGQGGYGGLGSQG-AGRGGLGGQGAG---
                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                       57.0%;
69.2%;
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-----GGLGGQGAGQGAGAAAAAAGGAGQGGYGGLGSQG
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Pred. No. 2.1e
12; Mismatches
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2.1e-121;
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Nephila.
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SEQUENCE OF 449-544 FROM N.A.
MEDLINE-98148687; PubMed-9487707;
Arcidiacono S., Mello C., Kaplan D., Cheley §
**Purification and characterization of recomb:
**expressed in Escherichia coli.**;
expressed from the expression of t
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046171;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
SPIDROIN 1 (FRAGMENT).
   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nephila clavipes (Orb spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
NCBI_TaxID=6915;
                                                         Submitted (JAN-1995)
EMBL; U20329; AAC3895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xu M., Lewis R.V.;
"Structure of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-90384959; PubMed-2402494;
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                                                                                                                                                         SEQUENCE
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                                                                                                                               Beckwitt
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                                   .w-1995) to the EMBL/GenBank/DDBJ
AAC38957.1; -.
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Best Local Similarity
Matches 406; Conserv
                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

COLGIN M.A., Lewis R.V.;

"Spider minor ampullate silk proteins or and highly conserved non-silk-like 'space protein Sci. 7:667-672(1998).

EMBL; AF027735; AAC14589.1; -.

InterPro: IPR000817; -.
                                                                                                                                                                                                                                                                                                       O17434 PRELIMINARY; PRT; 988 AA.
O17434;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MINOR AMPULLATE SILK PROTEIN MISP1 (FRAGMENT).
                                                                                                                                                                                                                  Nephila clavipes (Orb spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
NCBI_TaxID=6915;
  PRINTS;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                   076786 PRELIMINARY; PRT; 076786; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last seq 01-OCT-2000 (TrEMBLrel. 15, Last ann FIBROIN.
                                                                                                                                             Antheraea pernyi (Chinese oak silk moth).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Meoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Bombycoidea; Saturniidae; Saturniinae; Antheraea.
SEQUENCE FROM N.A.
Sezutsu H., Tamura
                                                                                                        Bombycoidea; Sat
NCBI_TaxID=7119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Badrock K., Basham D., Brown D., Chillingworth T., Connor R., A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Cliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E. Taylor K., Whitehead S., Barrell B.G.; The Complete genome sequence."; "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."; "Nature 393:337-544(1999)."
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O53559 PRELIMINARY; FRI, O53559; O1-JUN-1998 (TrEMBLrel. 06, Created) O1-JUN-1998 (TrEMBLrel. 06, Last sequence update) O1-JUN-2000 (TrEMBLrel. 14, Last annotation update) PGRS-FAMILY PROTEIN.
RV3514 OR MYV023.21.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Mycobacteriales; Corynebacterineae; Mycobacteriaceae; My
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InterPro; IPR000084; -.
InterPro; IPR002173; -.
Pfam; PF00934; PE; 1.
ProDom; PD001223; -; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_2.
SEQUENCE 1489 AA; 115754 MW; 6855CBA1C3CBAF3A CRC64;
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STRAIN-H37RV;
MEDLINE-98295987;
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NCBI_TaxID-1773;
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                                                                                   GAGQGGYGGLGSQGTSGRGGLGGQGA-------GAAAAAAAAAAAAGGA-------GQGG
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39.5%;
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RV3512 OR MTV023.19.
MEDLINE-98295987; PubMed-9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Children S., Seger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
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Mycobacteria; Firmicutes; Actinobacteria; Actinobacteridae

Bacteria; Firmicutes; Actinobacteria; Mycobacteriaceae;
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NCBI_TaxID=1773;
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ilarity 40.0%;
Conservative 7
              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1228.5; DB 2; Length 1079;
pred. No. 4.2e-72;
25; Mismatches 303; Indels 149;
              PRT;
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RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., RA Davies R., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., RA Davies R., Devlin K., Feltwell T., Gentles S., Murphy L., Alloyd S., Davies R., Devlin K., Krogh A., McLean J., Mule S., Murphy L., Alloyd S., Barrell M.A., Rajandream M.A., Rogers J., RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., RA Rutter S., Seger K., Skelton S., Squares S., Sqares R., Sulston J.E. Ray Taylor K., Whitehead S., Barrell B.G.; Toeciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. T; Rature 393:537-544(1998).

EMBL, ALO21942; CAAL7449.1; -.

EMBL, ALO21942; CAAL7449.1; -.

BR InterPro; IPR000209; -.

InterPro; IPR00020173; -.

PR Finn; PP00934; PE; 1.
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Best Local Similarity 38.1
Matches 325; Conservative
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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01-JUN-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
PGRS-FAMILY PROTEIN.
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PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_2.

PROSITE; PS00118; SUBTILASE_SER; UNKNOWN_1.

SEQUENCE 1306 AA; 105964 MW; 843A30955FFA56B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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      - AGAAAAAAAAAAGGA
                                                                      GKGGRGGTGGPGGAGPAGTTGSQGAGGNGGSGGTGGDPGDGGNGANGSVFTNNGIGGNGG
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                                                                                                                                                                                               GGDGGAAPNGVAGSQGPGGAGGDG--GTGGVGGNGGRGIDGADGATAGARGQDGGAGGAG
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Last sequence update)
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S
                                                            Query Match 33.9
Best Local Similarity 38.8
Matches 321; Conservative
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O53552;
O1-JUN-1998 (TremBLrel. 06, C
01-JUN-1998 (TremBLrel. 06, L
01-OCT-2000 (TremBLrel. 15, L
PGRS-FAMILY PROTEIN.
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EMBL; ALO22022,
HSSP; P00778; 2ULL.
Tuberculist; Rv3507; -.
Tuberculist; Rv3507; -.
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Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                  "Deciphering the biology of Mycobacterium complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-H37RY;
MEDLINE-98825987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J.
                                                                                                                                                              ProDom; PD001223; -; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_2.
SEQUENCE 1381 AA; 110624 MW; CA09676BD07F6482 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                                                         InterPro; IPR002173; Pfam; PF00934; PE; 1.
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PGGY-GPGQQTSG
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RV2490C OR MTV008.46C
                      MEDLINE-98295987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., GentLes S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quali A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,
Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:337-544(1998).
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InterPro; IPR000228; ...
InterPro; IPR000123; ...
Pfam; PP00934; PE; 1.
ProDom; PD001223; ...
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
PROSITE; PS01287; RTC; UNKNOWN_1.
SEQUENCE 1660 AA; 133124 MW; 3A889CE12COFA945 CRC64;
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GGAAPSGTVGSHGTGGVGGDGGLGGAGGVGGAGGNGGIGITVGGAGGAGGNGGDPG--AG 1158
                                                                                     AAAAAGGAGQGGYGGLGSQGTSGR------GGLGGQGAGAAAAAAAAAAAAGGAGQGGY 486
                                                                                                                                                      LGGQGAGAAAAAAAAAGGAGQ-------GGYGGLGSQG-TSGRGGLGGQ-GAGAAAAA 435
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                               GG-----LGSQGTSGPGGYG-----
                                                                  DGGAGGNGGAGGNGGVGASGGAGARGANGIDSIGGTGGAGGGGGGGGAGGVGGHGGDGGV 1100
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Qy	DЬ	Qy	Db	Qy	Oy	Db	Qy	Db	Qy	Db Qy	Query Best Match				RLS						000				A L	RESULT Q9NHW2	Db 1	Qy	Db 1	Qy	Db 1	Qy	Db 1	Qy
322 YGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGAG-AAAAAAAAAAAGGAGQGGYGGLGSQ 378	859 GGTTIIEDLDITVDGANGPITISEELTIGGAGAGGVGPGGSGPGGVGPGGSGPGGVGPGG 918	GRGG	9 GAGPSGAGPGGAGPSGAGRGGSGRGSVGRGGAGRGGAGGAGGAGGAGGSGAGGS	230 AAAAAAAAAGGAGQGGYGGLGS-QGTSGRGGLGGQGAGAAAAAAAAAAAAAGGA-GQGGYGGL 287	174 PGQQTSGRGGLGGQGAG-AAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAG-A 229	682 GPGGPYGPGGAGGPGGAGGPYGPGGPGGAGPGGYGPGGAGPGGAGPGGAGPGGYG 741	121 GGLGSQGTSGRGGLGGQGAGAAAAA-AAAAAGGAGQGGYGGLGSQGTSGPGGYG 173	AGGPYGPGGSGGPGGAGGPYGPGGAGGPYGP	70 AAAAAGGAGQGGYGGLGS-QGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGY 120	11 GSMASGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGS-QGTSGRGGLGGQGAGAAAAA 69	ry Match 33.2%; Score 1159.5; DB 5; Length 1884; it Local Similarity 39.7%; Pred. No. 1.8e-67; ches 318; Conservative 34; Mismatches 296; Indels 153; Gaps 35.	EQUENCE 1884 AA; 148/38 MW; 2/80F43339FUZUA3 CKC04;	1884 1884	EMBL; Arziboz3; AAr3o091.1; *. InterPro; IPRO00087; *.	ce 287:1477-1479(2000).	ar architecture	MEDLINE=20130/00; PODMED=10880/94; Hayashi C.Y., Lewis R.V.;	10000	I_TaxID=115969;	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachhida; Araheae; Araheomorphae: Entelegynae: Araheoidea: Tetragnathidae: Nephila.	ensis.	TAGE DULLEUR SIDE ERCIEIN (ERMOMENI).	01-MAR-2001 (TIEMBLIFE) 16, Last annotation update)	Created)	9NHW2 PRELIMINARY; PRT; 1884 AA.	10	337 NGGGTGQQGNGAAGGAGWSPDSDLKG 1364	645 AGQGGYGGLGSQGTSGPGGYGPGQQTSG 672	277 VAGGNGGAGGAGGAGGAFLGDGGNGGAGGQGGAGGGSPGGGGGVGGHGGAGGDAGM 1336	594GAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAA-AAAAAAAAAGG 644	GGAGGKGGDAGDI	544 TSGRGGLGGQGAGAAAAAAAAAAAGGA-GQGGYGGLGSQGTSGRGGLGGQGA 593	DSGNGTSAANGVDASKHGPLTGGDGGVGGNGAKAAAAGGDG	508 GRGGLGGQ

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RESULT 11
002402
ID 402402
AC 002402
DT 01-JUL
DT 01-JUL
DT 11-SOLU
DT 101-CCT
DE INSOLU
DT 01-CCT
CEURARY
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RN (1)
RP SEQUEN
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                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-97320490; PubMed-9177341;

Sudo S., Fujikawa T., Nagakura T., Ohkubo T., Sakaguchi K., Tanaka M., Nakashima K., Takahashi T.;

Nakashima K., Takahashi T.;

"Structures of mollusc shell framework proteins.";

Nature 387:563-564(1997).

REMBL; D86074; BAA20466.1; -.

EMBL; D86074; BAA20466.1; -.
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002402; PREMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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Pterioidea; Pteriidae; Pinctada.
NCBI_TaxID~50426;
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AAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQG--AGAAAAAAAAAAGGA 203
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                                                                    -----RGGLGGQGAGAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAA 145
                                                                                                                      SGRGGLGGQGAGAAAAAAAAAAAGGAG-----QGGYGGLGSQGTSG-----
                                                                                                                                                                                       SAGLYGVGGGGAWGAGGAGGADGGRGGGGGDWEYDYDDDSDDDDEWDWDDDDGGMGAGAG 120
                                                                                                                                                                                                                                                                                         Length 738;
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.	3 P.	
Parkhill J.;	RA C	
SEQUENCE FROM N.A.	R R	
L Nature 393:537-544(1998). N [2]	R RL	
	RT ?	
<pre>Taylor K., Whitehead S., Barrell B.G.;</pre>	RA	
Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,	RA	
Oliver S., Osborne J., Quail M.A., McLean D., Moute S., Marphy E.,	R RA	
7 7	R R	
,	RA S	
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,	R A	
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SEQUENCE FROM N.A. STRAIN-H37RV:	77 PF	
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Mycobacterium tuberculosis.	SO	
PGRS-FAMILY PROTEIN.	Ç DE	
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053395 PRELIMINARY; PRT; 1538 AA.	ID	
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679 -GSGGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	DЪ	
635 AAAAAAAAGGAGQGGYGGIGSQGYSGPGGYGPG 667	Qy	
629GGSAADVAAAAAAAAAMYGDGADGPDFDNGFGGGNGNGGGGGSGG-GGSGGG 678	Db	
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523 AAAAAAGGAGQGGYGGLGSQGTSGRGGLG-GQGAGAAAAAAAAAAAGGAGQGGYGGLGSQG 581	γQ	
536 RGGGSAAAAAAAAAAGGGWGGGMGGGFGVGLGGGFGGGFGG-GSSAAAA 585	Db	
463 GGQGAGAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGAGAAAA 522	Qy	
489 -GAGGGGTGGLGGLGGLGGGSAAAAAAAAAAAAASGGGGRALRRALRRQ 535	Db	
GRGGL 4	Qy	
LAAAGAGGGLGGGGGGGALAAALAAA 48	Db	
SGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Qy	
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GSQGTSGPGGYGPGQQT 34	Qy	
345 GGGGAAAAAAAAAAAASASRQMSGIRDALGDIKDLLRSNGASAKASAKASAVASTKS 404	Db	
260 LGGQGAGAAAAAAAAGGAGQGGYGGLGSQGTSGR 295	Qy	
GGGLGGVGFYGGRGGRRGRGRGG	дь	
204 GQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGG 259	Qy	
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                                                                                    GGQGAGAAAAA-----AAAAGGAGQGGYGGLGSQGTSGRGGL-----GGQGAGAAA-
                                                                                                                 SGGAGGNGGTGLNGAGGAGGAGGNAGVAGVSFGNAVGGDGGNGGNGGHGGDGTTGGAGGK 1314
                                                                                                                                               QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAA----AAAGGAGQGGYGGLGSQGTS-GRGGL
                                                                                                                                                                              GKGGNGGDG--GNVGLGGDAGSGGAGGNGGIGTDAGGAGGAGGAGGNGGSSKSTTTGNAG
                                                                                                                                                                                                                                      NGGLGGNGGVSETGFGGAGGNGGYGGPG--GPEGNGGLGGNGGAGGNGGVSTTGGDGGAG 1196
                                                                                                                                                                                                                                                         AAAAGG------AGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAGGAGQG
                                                                                                                                                                                                                                                                                                 GPGGAGDFASGVGGVGGAGGDGGAGGVGGFGGQGGIGGEGRTGGNGGSGGDGGGGISLGG
                                                                                                                                                                                                                                                                                                                    GPGGY----GPGQQTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLG
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DGGNGGNGGNSGNSTGVAGLAGGAAGAGGNGGGTSSAAGHGGSGGSGGGGTTGGAGAAGG
                                                        GGNGSSGAASGSGYVNYTAGHGGNGGNGGNGGNGSAGAGGQGGAGGSAGNGGHGGGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.1%; Score 1157; DB 2; ilarity 34.4%; Pred. No. 2.2e-67; Conservative 36; Mismatches 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GAGAAAAAAAAAAGG------AGQGGYGG-----LGSQGTS
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Best Local S
Matches 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nephila clavipes (Orb spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
NCBI_TaxID-6915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
FLAGELLIFORM SILK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00138; SÜBTILASE_SER; UNKNOWN_1
NON_TER 1 1
NON_TER 2249 2249
SEQUENCE 2249 AA; 174871 MW; 88C8B168A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF218621; AAF36090.1;
InterPro; IPR000087; -.
InterPro; IPR000209; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene.";
Science 287:1477-1479(2000).
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MEDLINE=20156766; PubMed=10688794;
Hayashi C.Y., Lewis R.V.;
"Molecular architecture and evolut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1435 NGGAGAGGGSLSTGQSGGPRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T MALCH 33.0%;
Local Similarity 36.7%;
hes 330; Conservative 30
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                                                                                                                                                                                                                                                                                                                                          GYGPGQQTSGRGGLGGQGAGAAAAAAAAAAAGGAGQG--GYGGLGSQGT-----SGR
                                                                                                                         -----GAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQ-GAGAAAAAAAAAAGGAG
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                                                                                         PGGYGPGGAGPGGYGPGGSGPGGYGPGGSGSGGYGPGGSGPGGYGPGGTGPGGSE
                                                                                                                                                                                                  GAGGPYGPGGAGGPYGPGGAG-GPYGPGGAGGPYGPGGAGGSYGLGGAGGSGGVGPGGSG
                                                                                                                                                                                                                                                                                                                GGVGTGGVGPGGAGGPYGPGGSGPGGAGSAG--GTYGPGGFGGPGGFGGPGGAGGPYGPG
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-AAAAAAAAGGAGOGGYGGLGS-----QGTSGRGGLGGQGAG-AAAA
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Pred. No. 7.5e-67;
0; Mismatches 288;
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                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 354; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galleria mellonella (Wax moth).
Eukaryota; Netazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Pyraloidea; Pyralidae; Galleriane; Galleria.
NCBI_TaxID=7137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9GUB5 PRELIMINARY; PRT; 1468 AA.
Q9GUB5;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HEAVY-CHAIN FIBROIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                       TISSUE-POSTERIOR SILK GLAND;
ZUROVEC M., Kodrik D., Yang C., Sehnal F.;
"Heavy-chain fibroin of Galleria mellonella L.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ da
EMBL; AF095239; AAG10393.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                AAAGSGASGVGGLGLSGLGPIGGIGPIGATSASTSGAGLGGVGAAGASGLGGLGGAGASA 386
                                                                                                                                                                                                                                     ASGRGGLGGQGA------GAAAAAAAAAAAAAAGGAGQ-----
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                                                                                                                                                                                                            ASGLGGLGGAGASAAGSAGAGLGGVGVGGSSGSSAASAASGASGAGEVILIDDRSSAASR 326
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                                                                                          AGSAGAGLGGIGAGGSSGSSAASAASGASGAGEVIVIDDRSSAASAAAASSGASGLGGLG
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                                                           SQGTSGRGGLGGQGAGAAAA - - AAAAAAGGAGQGGYGGLGSQGTSGRG - - -
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                                                                                                                                                                                                                                                                     32.9%;
ilarity 30.1%;
Conservative 7
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                                                                                                                                                                                                                                                                                                                                       1468
AA: 122705 MW;
                                                                                                                      GAAAAAAAAAGGAGQ------
                                                                                                                                                                                                                                                                     Score 1148; DB 5; pred. No. 8.2e-67; 78; Mismatches 215;
 AAAAAAAAGGAGQGGYGGLGSQGTSGP-GGYGPG
                                                                                                                                                                                                                                                                                                                                                2DA59E1181BB3DDF CRC64;
                                                                                                                                                                              -----GGYGGLGSQGTSGRGGLGGQGA--
                                                                                                                                                                                                                                                                                                                                                                                            databases
                                                                                                                                                                                                                                                                                                 Length 1468;
                                                                                                                                                                                                                                                                       Indels 528;
                                                            -GLGGQGAG
                                                                                                                      -GGYGGLG
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                                                                                                                                                                                                                                                      GPLGGTGPHGVSSASALGAGLGGVGAPGASGLGGLGVAGASAAGSAGAGLGGVGAGGSSG
                                                                                                                                                                                                                                                                       SGRGGLGGQGAGAAA--AAAAAAGGAGQGGYGGLGSQGTSGRG----GLGGQGAGAA-- 596
                                                                                                                                                                                                                                                                                                                                                                                       GAA-----AAAAAAAAAAGGAGQGGYGGLGSQGTSGP-GGYGP------
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                                                                                                                                                SALGAGLGGVGTAGASGLGGLGGTGASAAGSAGAG
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                                                                                                                                                                       AA--AAAAAAGGAGQGGYGGLGSQGTSGPGGYGPG
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                                                                                                                                                                                                                                                                                                                                  GQQTSGRGGLGGQGAGAAAA-------AAAAAAAGGAGQGGYGGLGSQGT
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O06810 PRELIMINARY; PRT; 1329 AA.

O06810; O1-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 107.4 KDA POTEIN.
PGRS-FAMILY OR RV1450C OR MTCY493.04.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 35.9
Matches 323; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000084; ...
InterPro; IPR002173; ...
InterPro; IPR003536; ...
Pfam; PF00934; PE; 1.
PRINTS; PR01370; TRNSINTIMINR.
PRODOM; PD001223; -; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 1329 AA; 107410 MW; 777A125F6DBAB
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; M.

NCBI_TaxID-1773;
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                                                 GNGANATVAGGAGGKGGNGGLVGNGGAGGKGGDGMAGVAGSSPTTAGESGTSGQNGG
                                                                                                                                                           GGNGAKGTFDNGGDGVGGNGGNGGSRGIGGAGGIGGAGSTAGADGARGATPTSGGNGGTG
                                                                                                                                                                                                             GGLGSQGT-----SGPGGYGPGQQTSGRGGLGGQGA-----
                                                                                                                                                                                                                                                                                                                                                                          GNGAPGAPPSGGDPNGGGGGAGGAGGKGGDGGAQAGDGGAGGAGGKGGNGGNGATGATGL 495
                                                                                                                                                                                                                                                                                                                                                                                                                            SQGT-----SGRGGLGGQGAGAAAAAAAAAGGA-GQGGYGGLGSQGTSGR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGQ--GGYGGLGSQGTS-GRGGLGGQGAGAAAAAAAAAAAGGA------GQGGYGGLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGGAGGPGPIGGVGGHGGVGGAAGLLGVGGHGGAGGHGAEGVAGAAGEDLSPHGTSGGVG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAAAAGG-AGQGGYGGLGSQ----GTSGRGGLGGQGAGAAAAAA------AAAA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGILWGNGGAGGSGAPGQVGGAGGAAGLFGTGGAGGAGGAGGAGGAGGAGGSGGWLLGNGGVG 198
                                                                                                      --GAAAAAAAAAGGAGQGGYGGL-GSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQ---
                                                                                                                                                                                                                                                                    NGLGAGADGTDGGKGGNGGAGGGGGAGGQGGKALAATHQDGSMGAGGAGGNGGAGGMGGD 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGSTIGAHGAAGASPTSGGNGGAGGNGAHFSSGGKAGGNGGAGGAGGLVGNGGAGGAG
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  -GGYGGLGSQ-----GTSGRGGLGGQGAGAAAAAAAAAAGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.8%; Score 1145; DB 2; 35.9%; Pred. No. 1.2e-66; Live 35; Mismatches 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107410 MW; 777A125F6DBAB234 CRC64;
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- ; - - - - AGQGGY
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                                                          LGGFGGNGAAGANGVAVGAPGQPGGAGGHGGAGGNGGAGGNGGQGVVSDGAGGAGGAGGD
                                                                           LGGQGAGAAAAAAAAAAGGAGQ----GGYGGLG------SQGTSGRGGLGGQ
                                                                                                                      GTGGNGGRGGDGAFGGMSANATNPGENGPNGNPGGNGGAGGAGGAGLNG-GNGGAGGNGG
                                                                                                                                                  GTSGRGGLGGQGAGAAAAAAA------AAAGGAGQGGYGGLGSQGTSGRGG
                                                                                                                                                                                  QGGSGGAGSTPGAKGAHGFTPTSGGDGGDGGNGGN----SQVVGGNGGDGGNGGNGGSA
                                                                                                                                                                                                             QGTSGPGGYGPGQQ-----TSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGL-GSQ
                                                                                                                                                                                                                                                                         GGL-----GSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYG---GLGS 491
                 - AGAAAAAAAAAGGAGQGGYGG-LGSQGTSGPGGYGPGQQTSGIRRPAAKL
                             680
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Search completed: July 3, 2001, 15:05:26 Job time: 591 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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      58.60.3
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SIDSB/gcgdata/geneseq/yeneseqp/AA1982.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:

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SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:

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|: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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11	16	11	18	21	22	22	17	22	22	17	21	19	12	19	16	9	21	18	14	19	19	14	22	22	21	18	17	11	9	20	16	20	16
AAR05309	AAW01496	AAR05312	AAW26350	AAY78286	AAB63999	AAB72729	AAR95109	AAB63997	AAB72727	AAR95107	AAY59071	AAW53347	AAR14309	AAW56163	AAR81318	AAP82962	AAY78283	AAW26348	AAR41013	AAW53524	AAW53518	AAR41007	AAB63995	AAB72725	AAY78277	AAW26342	AAR95105	AAR05307	AAP80940	AAY40103	AAR99059	AAY40099	AAR80168
SLP-L2 polymer (si	Silk-like protein	Sequence encoding	FCB-SLPIII (72 kDa	FCB-SLPIII amino a	SLP-C protein sequ	Repetitive protein	Silk like protein	FCB-SLP protein fr	Repetitive protein	Fibronectin cell b	N. clavipes spider	Nephila clavipes s	N.clavipes draglin	New DNA sequence i	Adhesion protein.	SEPL4 protein comp	4	SLP4 synthetic pro		Amino acid sequenc	Amino acid sequenc	Silk-like protein	SLPIII protein seq	Repetitive protein		Silk-like protein	Silk like protein	SLP III (Silk-fibr	SIPIII protein com	ĸ	ne v		Misp

ALIGNMENTS

06-JUL-1998

(first entry)

AAW53346

Nephila clavipes spider silk protein.

AAW53346 standard;

Protein; 718

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15-APR-1991;
20-APR-1990;
04-OCT-1994;
19-APR-1995;
                                                                                                                                                               Spider; Nephila clavipes; silk protein; tandem repeat; fibre; dragline; cocoon; tensile strength; elasticity.
               N-PSDB; AAV23249.
                      WPI; 1998-270437/24.
                                                                                                                    17-MAR-1998
Recombinant spider silk proteins - useful for making fibres
                                     Hinman MB,
                                                  (UYWY-) UNIV WYOMING
                                                                                                      19-APR-1995;
                                                                                                                                   US5728810-A.
                                                                                                                                                 Nephila clavipes
                                     Lewis RV,
                                                                 91US-0684819.
90US-0511792.
94US-0317844.
95US-0425069.
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                            GGLGSQGTSGPGGYGPGQQTSGIRIRAPSTS
                                                       qgag----aaaaaaggagqggygglggqgv-grgglggggag----
                                                                                    QGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGY
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ilarity 66.3%;
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Pred. No. 1.4e-145;
"""matches 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated DNA, vector and the production of spider
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20-APR-1990;
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                                                                                                                                                                                                                                                  QGAGAAAAAAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGGQGAG-AAAAAAAAAAAAAGGAGQ
                                                                                                      AGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAA------AGGAGQGGYGGLG
                                                                                                                                                    2000-061225/05.
DB; AAZ38195.
                                                          SQGTSGRGGLGGQGAGAAAAA----
                                                                                          g---aaaaaaaggagggggglgnqg-----agrgggg-----aaaaaa
                                                                                                                                                                                      ggygglgsqg----agrggqgag----aaaaaaggaggggggglgsqg-agrgglggqga
                      QGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGP-GQQTSGRGGL 350
qg----agrggegag---
                                            sqg-agrgglggqgagaaaaaaaggagqgglggqgagqgagasaaaaggagqggygglgs
                                                                                                                                                                                                                                                                                   498;
                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                            718 AA;
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90US-0511792.
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Pred. No. 1.4e-145;
20; Mismatches 49;
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                  The present sequence represents the natural spider silk protein spidroine major 1. The protein improves the moisturizing/softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spider silk protein; spidroine major 1; cosmetic; idermatological compositions; hair care; skin care; hormone; moisturizer; skin disorder; skin disorder
                                                                                                                                                                                                                                                                                     Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens -
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Matches 495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The spider silk protein contains a basic 34 amino acid repeat. The repeat itself contains 3 regions. The first comprises 0-9 amino acids with a sequence AGG(GX)2. This region is not highly conserved. The second region has a sequence AGG(A)x which is highly conserved and is 8-10 amino acids long. The third segment is (GGX)5 and is 15 amino acids long and is very highly conserved. In most cases X is A,O, Y or L. Remoyal of the poly-(Ala) segments results
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein superfibre;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; Page 23; 48pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                     encoding spider silk protein-1 and 2 and variants - isolated
n Nephila clavipes, for prodn. of spider silk protein and
res having desired characteristics
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              AAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGT
                                                                                                                                              GGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGP-GQQTSGRGGLGGQGAG
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Pred. No. 6.2e-145;
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This sequence represents a synthetic spider dragline variant polymer, CC DP-1A.9. The sequence of the DP-1A.9 monomer is given in AAR99052. CC The polypeptide monomer is a variant based on a consensus sequence CC derived from the fibre forming regions of spider dragline protein, ce esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. CC DNA sequence encoding the monomer may be used in the recombinant protein to production of the variant protein in a recombinant host, e.g. E. coli cor Bacillus subtilis. Synthetic analogues of DP1 were designed to mimic the repeating consensus sequence of the natural protein and the pattern CC of variation among individual repeats. DP-1A analogues are composed CC of a tandemly repeated 101 amino acid monomer which comprises four repeats which differ from the consensus sequence given in AAM06201, CC repeats which differ from the consensus sequence grove in AAM06201 (CC according to the pattern (1)-(5) given below. This 101 amino acid conditions in a series of analogue proteins. The pattern:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DP-1A analogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR99053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fahnestock SR;
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orming region; Spidroin 1; Nephila clavipes; DP1; r
orming region; Spidroin 1; Nephila clavipes; DP1; r
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGP-GQQTSGRGGLGGQGAGAAAAA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qgagrggqgagaaaaaaggagqggygglgsqgagrgglggqgagaaaaaaaggagqgglg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGA---GAAAAAAAAAGGAGQGGYGGLGSQGT--SGPGGYGPGQQT-----SGRGGLG 187
                                                                                                                                                                                                          AAGGAGOGGYGGLGSQCT--SGRGGLGGQGA---GAAAAAAAAAAGGAGQGGYGGLGSQG
                                                                                                                                                                                                                                                  GRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGGQGA---GAAAAAA 476
                                                                                                                                                                                                                                                                                                                                                                         aaaaaaggagggggglgsqg-agrgglggggg---aaaaaaaggagq------
                                                                                                                                                                                                                                                                                                                                                                                       AAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                 qgagqgagaaaaaaggagqggygglgsqg----a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agqggygglgsqg-agrgglggqgag---aaaaaaaggagq------gglgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQGAGAAAAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGGQGA---GAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  grggqgag----aaaaaaggagqggygglgsqg-agrgglggggag---aaaaaaaggag
                                                                                      AGGAGQGGYGGLGSQGTSGPGGYG 667
                                                                                                                                                               TSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAA
                                                                                                                                                                                       aaggagqggygglgsqgagqggygglgsqgagrggqgagaaaaaggagqggygglgsqg
                                                                                                                                                                                                                                                                                                             --gglgsqgagagaaaaaaggagqggygglgsqgaggggggggggggagaa
                                                                        aggagqggygglgsqg-agqggyg
                                                                                                                                -agrgglgggggg---aaaaaaaggagg----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is generally preceded by a repeat containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        606 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -gglgsqgagqagaaaaaaggagggggglgsqgaggggggglgs 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.6%;
69.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2076;
Pred. No. 3
                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 16;
3.2e-141;
                                                                                                                                 gglgsqgagqgagaaaa
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AAY40100 standard; protein;

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                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 477; Conserv
                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a polymer of an analogue of the spider silk protein spidroine major 1. The protein improves the moisturizing/softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins, hormones, moisturizers or agents for treating disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spider silk protein; spidroine major 1; cosmetic; n dermatological compositions; hair care; skin care; hormone; moisturizer; skin disorder; skin disorder
                                                                                                                                                                                                                                                                                                                                                        skin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Philippe M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1999
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                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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               243
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                                                                                              101
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                                                                                                                                                                                                                               21 GLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAG
                                                                                                                                                                                                      3 grggqgag----aaaaaaggagqggygglgsqg-agrgglggqgag---aaaaaaaggag
AGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAGGAGGGYGGLGSQGTSGRGGLGG
                                                                                                            QGA---GAAAAAAAAAGGAGQGGYGGLGSQGT--SGPGGYGPGQQT-----SGRGGLG
                                                                                                                                                               QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGG
                                                                   GQGAGAAAAAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGGQGA---GAAAAAAAAAAAAGG
                                                                                          qgagrggqgagaaaaaaggagqggygglgsqgagrgglggqgagaaaaaaggagqgglg
                                                                                                                                               sqgagqgagaaaaaggagqggygglgsqgagqggygglgsqgagrgggggagaaaaagg
                                                                                                                                                                                                                                                                                                                                                        hair.
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                                                                                                                                                                                                                                                                                                                              606 AA;
                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garson JC,
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1..101
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                                                                                                                                                                                                                   58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "monomer unit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arraudeau JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spider silk protein spidroine major 1.
                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                         Score 2076; D
Pred. No. 3.2e
11; Mismatches
                                                                                                                                                                                                                                                                        .2e-141;
                                                                                                                                                                                                                                                                                     DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           make-up;
                                                                                                                                                                                                                                                           Indels 122;
                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sunscreen;
                                                                                                                                                                                                                                                           Gaps
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RESULT

AAW271178

ID AAW2

XX AAW2

AC AAW2

AC AAW2

AC AAW2

XX Neph

KW H1gh

KW H1gh

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KW G1av

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          A process has been developed for the production of a DNA fragment encoding slik protein. The process involves: (a) selecting target DNA, from a silk-producing spider, that contains many repetitive and non-repetitive regions; (b) selecting a single-stranded DNA primer of at
                                                                                                                                                                                                                                                                                                    WPI; 1997-179272/16.
N-PSDB; AAT85356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High strength film; fibre; woven article; parachutes; sails; absorber; body armour; heavy metal; biological weapon; chemical; flavour; fragrance; Nephila clavipes.
                                                                                                                                           Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                               (BASE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nephila clavipes spider silk
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high
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                                                                                                                                                                                                                                                                                                                                                                                                                               BASEL
                                                                                                                                                                                         multimerised DNA sequences encoding spider silk protein oth repetitive and non-repetitive sequences, useful for igh strength films, fibres, woven articles etc.
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                                                                                                                                        Fig 1; 57pp;
                                                                                                                                                                                                                                                                                                                                                                            Elion GR;
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                                                                                                                                           English.
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Best Local
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-saaasrlsspqas
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Pred. No. 5.6e-140;
8; Mismatches 58;
   557
                                 683
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RESULT AAR99055 ID AARS

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AAR99055

standard;

Protein;

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                                                                                                                                                  This sequence represents a synthetic spider dragline variant polymer, CC DP-1B.9. The sequence of the DP-1B.9 monomer is given in AAR99054. CC The polypeptide monomer is a variant based on a consensus sequence cc derived from the fibre forming regions of spider dragline protein, CC esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. The CC DNA sequence encoding the monomer may be used in the recombinant CC production of the variant protein in a recombinant host, e.g. E. coli CC or Bacillus subtilis. Synthetic analogues of DP1 were designed to mimic CC the repeating consensus sequence of the natural protein and the pattern of variation among individual repeats. This monomer exhibits all of the regularities of (1)-(5) below. In addition, it exhibits a regularity of the natural sequence which is not shared by DP-1A, namely that a repeat CC in which both GYG and GRG are deleted by DP-1A, namely that a repeat CC in the natural sequence of DP-1B matches the natural sequence more closely over CC a more extended segment than does DP-1A. The individual repeats differ CC a more extended segment than does DP-1A. The individual repeats differ CC in the consensus sequence given in AAM06201 according to the pattern: CC consensus sequence given in AAM06201 according to the pattern: CC (1) the poly-alanine sequence varies in length from 0-7 cC (3) aside from the poly-alanine sequence, deletions usually CC encompass integral multiples of three consecutive residues; (4) deletion of GYG is generally accompanied by deletion of GRG in the same sequence; and
                                        Query Match
Best Local Similarity
Matches 462; Conserv
                                                                                                                                                                                  The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
                                                                                                                                                                                                                                                             in the same sequence; and (5) a repeat in which the entire poly-alanine sequence is deleted is generally preceded by a repeat containing six alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spider; dragline protein; variant; monomer; polymer; fibre forming region; Spidroin 1; Nephila clavipes; DB; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope; surgical suture; implant; reinforcement; film; coating.
                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 88-90; 168pp; English.
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GAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLG
                                                                                                                                             606 AA;
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                                        Score 1972.5;
Pred. No. 7.8e
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7.8e-134;
nes 35; In
                                           Indels 215;
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             13-AUG-1999
                                                                                                                                                      Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscre hormone; moisturizer; skin disorder; skin disorder.
                                                                                                                                                                                                                                                                                    AAY40102 standard; protein;
                                                                                                                                                                                                                                  19-NOV-1999
                                      FR2774588-A1
                                                                         Peptide
                                                                                                                              Synthetic
                                                                                                                                                                                                         Polymer of an
                                                                                                                  Nephila clavipes
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                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens
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                              LGSQGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAAAAAAGGAGQGGYGGLGSQGT----
                                                                           AGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGG
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                                                                                                                                                                                                                                                                                GYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGP-GQQ
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                                                                                                                                                        SGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGT-----SGRGGLGGQG
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Pred. No. 7.8
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                                                                                                                                                                                                                                                           This sequence represents a synthetic spider dragline variant polymer, CC The polypetide monomer is a variant based on a consensus sequence CC derived from the fibre forming regions of spider dragline protein, CC esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. The CC MA sequence encoding the monomer may be used in the recombinant CC production of the variant protein in a recombinant host, e.g. E. coli CC production of the variant protein in a recombinant host, e.g. E. coli CC the repeating consensus sequence of the natural protein and the pattern CC of variation among individual repeats. This monomer exhibits all of the CC regularities of (1) (5) below. In addition, it exhibits a regularity of CC the natural sequence which is not shared by DP-1A, namely that a repeat CC in which both GVG and GRG are deleted is generally preceded by a repeat cacking the entire poly-alanine repeat, with one intervening repeat. The sequence of DP-1B matches the natural sequence more closely over a more extended segment than does DP-1A. The individual repeats differ CC a more extended segment than does DP-1A. The individual repeats differ CC (1) the poly-alanine sequence varies in length from 0-7 called in the consensus sequence given in AANO6201 according to the pattern: CC (1) the poly-alanine sequence varies in length from 0-7 called in the consensus sequence given in AANO6201 according to the pattern:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rope;
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DP-1A analogue; fibre; high tensile strength; elasticity; cloth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR99057;
                            in the same sequence; and (5) a repeat in which the entire poly-alanine sequence is deleted is generally preceded by a repeat containing six alanine
                                                                                                                                                                                                                                         so also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 106-108; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-036479/05
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                        (5)
                                                                                                                 residues; (2) when the entire poly-alanane sequence is the surrounding sequence encompassing AGRGGGGGAGANGG; (3) aside from the poly-alanine sequence, deletions usualliss integral multiples of three consecutive residues; (4) deletion of GYG is generally accompanied by deletion (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dragline protein; variant;
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Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscreen; hormone; moisturizer; skin disorder; skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
                                                       Polymer of an analogue of spider silk protein spidroine major
                                                                                                                                          AAY40101 standard;
                                                                                     19-NOV-1999
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                                                                                                                                                                                                                                        AAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAGGAGQGGYGGLG 656
                                                                                                                                                                                                                                                                    gglgsqgagqggygglgsqgagrgglggqgagaaaaaaaaggagqgglgsqgagqagaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YGGLGSQGTSGPGGYGP-GQQTSGRGGLGGQGAGAAAA------A 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sqgagqgagaaaaaaggagqggygglgsg----agrggqgag----aaaaaaggagqgg
                                                                                                                                                                                                                                                                                                                                                                                  aaggagqggygglgsqg-agqggygglgsqgagrgglggqgagaaaaaaaggagqgglgs
                                                                                                                                                                                                                                                                                                                                                         ----AAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGY
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                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                         -SGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGA 305
                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.6%;
                                                                                                                                          909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1971.5; DB 16; Length 604
Pred. No. 9.2e-134;
B; Mismatches 37; Indels 207;
                                                                                                                                          ₹
                                                                                                                                                                                                                                                                                                                                           ---- AAA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a polymer of an analogue of the spider silk protein spidroine major 1. The protein improves the moisturizing/softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins, hormones, moisturizers or agents for treating disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cosmetic for hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Philippe M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-1998;
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  319
                                                                                                                                                              198 AAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAAAAGGAGQGGYGGLGSQGT-
                        344 TSGRGGLGGQGAGAAAA-----
                                                                                                                                                  156
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                                                                                                                                                                                                                                                    45 sqgagqgagaaaaaaggagqggygglgsqg----agrggqgag----aaaaaaggagqgg
                                                                                                                                                                                                                                                                                                                               40 GAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLG
                                                                                                                                                                                                                                                                                                     3 gagqggygglgsqg-agrgglggqgag---aaaaaaaggagq------gglg
                                                              gagrgglggggagaaaaaaaggagggglgsggaggagaaaaaaggaggggggglgsqg-
                                                gygglgsqg----agrggqgag----aaaaaaggagqggygglgsqg-agqggygglgsq
                                                                                               qggygglgsqgagrgglggagaaaaaaggaggglgsqgaggagaaaaaaggagqg
                                                                                                                                               aaaaaggaggggggglgsqg----agrggggag----aaaaaaggaggggggglgsqgag
                                                                                                                                                                                                 ygglgsqg-agqggygglgsqgagrgglggqgagaaaaaaggagqgglgsqgagqgaga
                                                                                                                           -----SGRGGLGGQGAGAAAA-----
                                                                                                                                                                                                                                                                                                                460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clavipes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or dermatological composition containing spider silk or skin care, in make-up or sunscreens -
                                                                                                                                                                                                                                                                                                                                                                                                                                             hair.
                                                                                                                                                                                                                                                                                                                                                                                                                    606 AA
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5B; 32pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garson
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                                                                                                                                                                                                                                                                                                                                                                 55.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arraudeau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          make-up
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8
                                                                                                                                                                                                                                                                                                                                                                  Score 1963.5; DB 20; Pred. No. 3.4e-133;
                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                           -----AAAAAAGGAGQG
                           --AAAAAAGGAGQGGYGGLGSQGT
                                                                                                                                                                                                                                                                                                                                                        35
                                                                                                                                                                                                                                                                                                                                                        Indels 215;
                                                                                                                                                                                                                                                                                                                                                                              Length 606;
                                                                                                                                                                                                                           A----A
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                                                                                                                                                                                                                                                                                                                                                        Gaps
                           382
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ARRESULT 1
AARROLLS A
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                        This sequence represents the product of cDNA clone, pMISS1, encoding the orb web spider minor ampullate silk protein MISP1 has been identified and sequenced. Repeat unit peptides of MISP1 may form part of a larger polypeptide with an amino terminus (see AAR80184-85) and a carboxy terminus (see AAR80186-89). Repeat unit peptides make upspider silk proteins (spidroins) which in turn aggregate to form the silk fibres. Spider silk fibres have high tensile strength and significant elasticity. An isolated cDNA clone of a silk protein encoding sequence is of use to produce the protein at high yields
                                                                                                                                                                                                                                                                                                                                          Polypeptide(s) comprising repeated unit amino acid sequences, cDNAs - derived from minor ampullate spider silk proteins and to form spider silk fibres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spider silk; repeat unit; consensus; minor ampullate silk protein;
spidroin; MiSP; orb web spider; dradline
                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYWY-) UNIV WYOMING
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     recombinant DNA technology.
                                                                                                                                                                                                                                                                                          2; Fig 1; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MisP spider silk protein insert product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ98470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lewis RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0209747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "represented as indeterminate,
to a highly compressed GC ricl
AAQ98470 which could not be so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        831
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Best Local
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                              Spider silk protein; spidroine minor 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscrehormone; moisturizer; skin disorder; skin disorder.
                                                                                                                            AAY40099;
         Nephila clavipes
                                                                               Spider silk
                                                                                                      19-NOV-1999
                                                                                                                                                   AAY40099 standard; protein;
                                                                                                                                                                                                            683
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                                                                                                                                                                                                                        GSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYG
                                                                                                                                                                                                                                                                                                                   QTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYG---GLGS-----QGTSGRGGLG-GQGA
                                                                                                                                                                                                                                                                                                                                                                                                               GAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gygrgagagagaa--gagaggygggggygagagagaaaaaagagsggaggygrgagaga
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                                                                                                                                                                                                                                                                               GAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGL
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                                                                                                                                                                                                                                                                                                     srggragaagagaaagagagaggygggggggagagaaaaagagsggaggygrgaga
                                                                                                                                                                                                                                                                                                                                                    349;
                                                                                                                                                                                                                                                                                                                                                                           -GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGG---LGSQGTSGPG-GYGPGQ
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50.1%;
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                                                                                                                                                    615
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                                                                               minor 1.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the natural spider silk protein spidroine minor 1. The protein improves the moisturizing/softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins, hormones, moisturizers or agents for treating disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                             SGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQG
                                                                                                                                                                                                                                              GAGQGGYG-----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGT
                                                                                                                                                                                                                                                                                       RGGLGGQGAGAAAAAAAAAGGAGQGGYG-GLGSQGTSGRGGLGGQGAGAAAAAAAAAAG
                                                                                                                                                                                                                                                                                                                            aagagaggyggggggagagaaaaaaagagsggaggygrgagagagaaagagag--ags
                                                                                                                                                                                                                                                                                                                                           AAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAA--AGGAGQGGYGGLGS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                      gaggygrgaggyggggggagagaaaaagagaggaggy-----grgagaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRGSMASGRGGLGGQGA-GAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAA
aagagagaaagagagaggygggggggagaragaaaaagagaggaagysrggragaagaga
                                                                                                                                                                                                                  LGGQGAGAAAAAAAAAAGGAGQGGYGG---LGSQGTSGPG-GYGPGQQTSGRGGLGGQGA
                                                                               GGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYG-GLGSQGTSGRGG
                                                                                                       rgagagagaa--gagaggygggggygagagaaaaatgaggaggygrgagagagaaag
                                                                                                                                    AGAAAAAAAAAAGGAGQGGYGGLGSQG-----TSGRGGLGGQGAGAAAAAAAAA
                                                                                                                                                                                                                                                                        -grg--agagagaaagagagaaagagaggygggggyg-agagagaaaaagagaggaggyg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Fig 3; 32pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1400; DB 20;
Pred. No. 5.5e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 120;
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                                                     437
                                                                               463
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RESULT 1
AAR99059
ID AAR99059
XX AAR9
XX Spld
XX POP-1
XX POP-1
XX POP-1
XX PP 15-0
XX PP 15-0
XX WPI
XX WPI
XX WPI
XX WPI
XX WPI
XX WPI
XX Dis
CC DP-
CC DP-
CC DP-
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CC PT
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                                        differ from the consensus repeat sequence by deletions of integral multiples of five consecutive amino acids consisting of the pentapeptide sequences GPGGY or GPGQQ. Synthetic analogues of DP2 were designed to minic the repeating consensus sequence of the natural protein and the pattern of variation among individual repeats. The analogue DP-2A is composed of tandemly repeated 119-amino acid peptide monomers which comprises three repeats which differ according to (1)-(2) above. This 119 amino acid monomer is repeated 1-16 times in the DP2 analogues. The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a synthetic spider dragline variant polymer, DP-2A. The sequence of the DP-2A monomer is given in AAR99058. DP-2 has a repetitive sequence and is rich in Gly and Ala. It is unlike DP-1 except for the region of consecutive Ala residues. The repetitinature of the protein and the pattern of variation lead to the production of the consensus sequence given in AAR99085. The individual repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus sequence according to a pattern while repeats differ from the consensus according to the consensus according to the consensus according to the consensus according to
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                                                                                                                                                        AAY40103 standard;
                                                             Polymer of an analogue of spider silk protein spidroine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
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Search completed: July 3, 2001, 14:58:11 Job time: 441 sec

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Minimum DB seq length: 0
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1: /cgn2_6/ptodata/2,
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3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                      US-08-425-069-2
US-09-317-8448-2
US-09-034-177-3
US-09-0458-298-2
US-08-458-298-2
US-08-475-598-64
US-08-477-5098-64
US-08-475-411A-31
US-08-478-029A-3
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-2 -2 Application US/08425069		30.5	30.6	30.8	30.8	30.8	30.8	31.0	31.0	31.0	31.1	31.2	31.2	31.2	31.2	31.4	31.4	31.4	32.0	
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		Sequence 2, Appli	Sequence 28, Appl		Sequence 61, Appl	•	•	11,	13	6	201	Sequence 51, Appl		Sequence 80, Appl	•	16,	•	•	•	

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25 QGAGAAAAAAAAAAGGAGQGGYGGLGSQGT--SGRGGLGGQGAG-AAAAAAAAAAAAGGAGQ 81

Query Match
Best Local Similarity 66.3
Matches 498; Conservative

60.3%; Score 2138; DB 1; 66.3%; Pred. No. 3.5e-147; tive 20; Mismatches 49;

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US-08-317-844B-2
                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08317844B Patent No. 5989894
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                            NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
CORRESPENDINGE ADDRESS:
STREET: 301 No. 5999894th Washington Street
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                      APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Yu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                  STATE: Virginia COUNTRY: U.S.A. ZIP: 22046
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LENGTH: 718 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-317-844B-2
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Best Local (
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TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
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REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/317,844B FILING DATE: 04-OCT-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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| GGYGGLGSQG----AGRGGQGAG----AAAAAAAGGAGQGGYGGLGSQG-AGRGGLGGQGA 107
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     QGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGY 652
                                                                                                         GGYGGLGSQGAGR----GGQGAGAAAAAAVGAGQEGIRGQGAGQGGYGGLGSQG-SGRGGL
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                                       GGQGAGAAAAAAGGAGQGGLGGQGAGQGAGAAAAAAGGYRQGGYGGLGSQG----AGRGG
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(703) 241-2848
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Best Local Similarity 66.3%;
Matches 498; Conservative 2
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,177
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN FIBROUS PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: PRIOR APPLICATION DATA:
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NAME: Billings, Lucy J
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CITY: P
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               G---AAAAAAAGGAGQGGYGGLGNQG---
                                                                       GGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAGGAGGGGGGGGGGGGGGGTSGRGGLGGQGA 141
                                                                                                                    QGAG----AAAAAAGGAGQGGYGGLGGQGAGQGGYGGLGGQGAGAAAAAAAAGGAGQ 56
                                                       GGYGGLGSQG----AGRGGQGAG----AAAAAAGGAGQGGYGGLGSQG-AGRGGLGGQGA 107
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Pred. No. 3.6e-147;
0; Mismatches 49;
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       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,747
FILING DATE: 14-MAR-1994
CLASSIFICATION: 530
ATTORNEY_AGENT INFORMATION:
NAME: MUIPHY JT., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-104P
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider TITLE OF INVENTION: Silk Proteins
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lewis, Rando
APPLICANT: Colgin, Mark
                                                                                                                                                                                                                                      STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
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                                                                                                                                    Release #1.0, Version
            28,977
ER: 1447-104P
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703-205-8050

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; NAME/KEY:
; LOCATION:
US-08-209-747-2
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Best Local Similarity
Matches 349; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: N. Clavipes
TISSUE TYPE: minor ampullate gland
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                617 LGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYG 653
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                                                                                                                                          QQTSGRGGLGGQGAGAAAAAAAAAGGAGQGGYG---GLGS-----QGTSGRGGLG-GQG 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQGAGAAAAAAAAAGGGGQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQCAGAAAAA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGG 616
                                                                                                                                                                                                                                                    YGRGAGAGAGAAAGAGAGTGG-----AGYGGQGGYGAGAGAAAAAAGAGAGAGY
                                                                                                                                                                                                                                                                                  QGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGY 450
                                                                                                                                                                                                                                                                                                                 AAGAGAGGAGGYGRGAGAGAAAA--GAGAGGYGGQGGYGAGAGAAAAAAATGAGGAGG
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                                                                                                                       YSRGGRAGAAGAGAAAAAGAGAGAGAGAGAGAGAAAAAAGAGSGGAGGYGRGAG
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-RGAGAGGYGGGGGGAGAGAAAAA--GAGAGGYG
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; Pred. No. 2.1e-94;
17; Mismatches 207;
                                                            -GGQGGYGAGAGAAAAAGA--GAGRGGYG-
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RESULT

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Best Local Similarity
Matches 349; Conserva
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APPLICANT: Lewis, Rando
APPLICANT: Colgin, Mark
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: ii
ORIGINAL SOURCE:
ORGANISM: N. C
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-104P
TELECOMMUNICATION INFORMATION:
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FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                            198 AAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAA------AAAAAG 241
242 GAAAGAGAGAGSYG
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                    GYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYG-----GLGSQGTSGRGGLG 137
                                                                                                                                                                                                       GGYGAG---AGAVAAAGAAGAGGYG----RGAGGYGGQGGYGAGAGAAAAA--GAGAG 129
                                                                 GYGRGAGAGAAA--GAGAGGYGGQGGYGAGAGAGAAAAAAGAGSGGAGGYGRGAGAGA 241
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P.O. Box 747
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------GQGYGAGAGAGAAAAXXXXXXXXXXXXXXXXXGAGAGAG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                            39.7%; Score 1405; DB 1; 50.1%; Pred. No. 2.1e-94; tive 17; Mismatches 207
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                                                                                                                                                                                                                                                                                                                Length 832;
                                                                                                                                                                                                                                                                                   Indels 124;
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US-07-609-716-31
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                                                           TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
                                                                                                                     FILING DATE: 06-NOV-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETTERM I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-5:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Ferrar
APPLICANT: Cappel
TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: prote
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 06-NOV-199
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
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CITY: San Francisco
STATE: CA
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                                                                                                                                                                                                                       RESULT
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                                                                                                                                            Sequence 29, Application US/08175155 Patent No. 5641648 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.0
Best Local Similarity 40.3
Matches 292; Conservative
               APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W.
APPLICANT: Dorman, Mary A.
TITLE OF INVENTION: Methods fc
TITLE OF INVENTION: Repetitive
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                               666 YGPG 669
                                                                                                                                                                                                                                                                                                                                                                                                                           65 AGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAA 724
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                                                                                                                                                                                                                                                                            788
                                                                                                                            Ferrari, Franco A.
               Methods for Preparing Synthetic Repetitive DNA: 69
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; MOLECULE TYPE: peptide US-08-175-155-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-398-3249
NFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 AGGAGQG--GYG-----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLG 164
                                                                                                                                                                                                                                                                        425
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  499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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CLASSIFICATION:
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                                                                                                                                                                SGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS
                                                                                                                                                                                                                                                                        GSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 484
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PGGYGPGQQT---SGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG---GL 552
                                                     GAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 604
                                                                                                        GQGGYG-----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAAGGAGQGGYGGLGSQGTSG 498
                                                                                                                                                                                                                -GLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGA 445
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US-08-477-509B-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                        TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dorman, Mary A TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding
                                                                                                                                           REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                          FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Relaction CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
MOLECULE TYPE:
                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 07-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 22-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 04-NOV-1986
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/114,618 FILING DATE: 29-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                      TOPOLOGY:
                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94111
                                                                                                                                                                                                          Trecartin, Richard F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Flehr, Hohbach, Test, Albritton & Herbert Four Embarcadero Center, Suite 3400
                                                                          1177 amino acids
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                        linear
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SYSTEM: PC-DOS/MS-DOS
   peptide
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Query Match Best Local Similarity

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: Sequence 35, Application US/08707237A

: Patent No. 5830713
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                                                                                                                                                                                              GENERAL INFORMATION:
                                               APPLICANT: Dorman, Mary A.
TITLE OF INVENTION: METHODS FOR PREPARING
TITLE OF INVENTION: REPETITIVE DNA
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                            APPLICANT: Ferrari, Franco A. APPLICANT: Capello, Joseph APPLICANT: Crissman, John W. APPLICANT: Dorman, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         613
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                                  ADDRESSEE:
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 San Francisco
                  E: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
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                                                                                                           SYNTHETIC
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-DEC-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 22-APR-19
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-10/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-NOV-1986 ATTORNEY/AGENT INFORMATION: NAME: Trecartin, Richard F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 09-NOV-PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                   114 AGGAGQG--GYG------GLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLG
279 GGAGQGGYG-----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQG
                                                                                                                                                                                                                                                                                         125 SGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/114,618 FILING DATE: 29-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                  67 AAAAAAAAAG------GAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAA 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                         GAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG
                                                                             G---GLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAA 278
                                                                                                                           AGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGA 304
                                                                                                                                                                SQGTSGPGGYGPGQQT---SGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGR 221
                                                                                                                                                                                                           GAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 64, Application US/08482085B Patent No. 6018030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                          COMPUTER READABLE FORM: 
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Richardson, Cna.
APPLICANT: Richardson, Cna.
APPLICANT: Chambers, James
Stuart
             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 22-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W.
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
NUMBER OF SEQUENCES: 112
                                                                                    APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,085B
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESSE: Flehr, Hohbach, Test, Albritton & Herbert
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                         APPLICATION NUMBER: US 07/114,618 FILING DATE: 29-OCT-1987
                                                                                                                                                  FILING DATE: 0: CLASSIFICATION:
                                                                                                                                                                                                                                                                                       COUNTRY: U
                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGAG 788
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 APPLICATION DATA:
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Pollock, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrari, Franco A.
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                              US 08/053,049
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Best Local Sin
Matches 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-398-3249 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME:
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YGPG
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                669
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114 AGGAGOG--GYG-----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGLG
                                    GYG-----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGG 665
                                                                                                                                             GGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAAGGAGQG 612
                                                                                                                                                                                                                                                                      PGGYGPGQQT---SGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG---GL 552
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GYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAG
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                                                                                                                  AGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGA 445
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Pred. No. 1.6e-82
58; Mismatches 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NOTION.

APPLICATION NOTION:

FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard F.

REGISTRATION NUMBER: 31.801
REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK
TELEPHONE: 415-781-1989
TELEPHONE: 415-781-1989
TELEPAX: 415-384-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
COMPUTER: CH
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,411A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 29-CCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-CCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-CCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
                                                                                                                                                                                                                                                                                                                 Query Match 35.0%; Score 1241.5; DB 4; Length 1177; Best Local Similarity 40.3%; Pred. No. 1.6e-82; Matches 292; Conservative 58; Mismatches 313; Indels 61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/08475411A Patent No. 6140072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
                                                                                                       125
185 GAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 244
                                               114 AGGAGGG--GYG-----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400 CITY: San Francisco STATE: CA
                                                                                                                                                         67
                                                                                                                                                                                                               65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                   AAAAAAAAAG------GAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAA 113
                                                                                                                                                                                                         GSGAGAGSGAAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 124
                                                                                                                                                                                                                                                         GQQMGRGSMASGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAG 66
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Qy	165	SQGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGR 221
Ъ	245	GSGAGAGSGAGAGSGAGAGSGA
Db Qy	222 305	GGLGGQGAGAAAAAAAAAAAAAAAA 278 :
Qy	279	GGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQG 331
Ъ	365	AGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGA 424
Qy	332	TSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG 386
Ъ	425	GSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 484
Qy	387	4
рь	485	SGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 544
Qy	446	GQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSG 498
В	545	GAAGYCAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
VΩ	499	PGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGL 552
Ф	605	AAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGA 664
Qy	553	GGQGAGAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQG 612
Ф	665	GAGSGAGAGSGA
Qy	613	GYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGG 665
ф	725	GYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAG 784
Qy.	666	YGPG 669
рb	785	YGAG 788
RESULT	T 12 -478-)29A-31
; Sec	t en	
; ; G	APPLIC	INFORMATION: CANT: Ferrari, I
•• ••	APPLI	CANT: Cappello, Joseph OF INVENTION: Functional
	TITLE	OF INVENTION: Synthetic Protein Polymer
** **	CORREST	ONDENCE ADDRESS:
	ADD	ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
• •• •	CITY:	an Francisco
٠. ٠.	COU	TRY
•• ••	COMPUTER	TER READABLE FORM:
٠. ٠.	COM	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
	OPE	SYSTEM:
```	CURRE	ATA:
*. *.	FIL	7. BE
٠. ٠.	PRIOR	æ. 0
	APP	APPLICATION NUMBER: US 07/609,716

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

US 07/269,429

FILING DATE:

09-NOV-1988

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US-08-478-029A-31
 Query Match
 TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
 PRIOR APPLICATION DATA: US 06/927,258
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
 MOLECULE TYPE: protein
 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 485
 222 G---GLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAA 278
 245
 185 GAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
 114 AGGAGOG--GYG-----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLG 164
 watch 35.0%; Score 1241.5; DB 4; Local Similarity 40.3%; Pred. No. 1.6e-82; nes 292; Conservative 58; Mismatches 313;
 STRANDEDNESS: single TOPOLOGY: linear
 LENGTH: 1177 amino acids TYPE: amino acid
 REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-8/RFT/MTK
 NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801
 67 AAAAAAAAAAG------GAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAA 113
 7 GOOMGRGSMASGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAG
 TSGPGGYGPCQQT---SGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG-- 386
 AAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGA
 GYG-----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGG
 GGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQG 612
 PGGYGPGQQT---SGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG---GL 552
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 GQGGYG-----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSG
 SGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS
 GSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG
 GGAGQGGYG-----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQG 331
 GAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG
 AGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGA 304
 SGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 184
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 AGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAA 724
 -GLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGA 445
 DATE: 29-OCT-1987
 US 07/114,618
 Length 1177;
 Indels
 61; Gaps
 484
 124
 665
 664
 604
 498
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 364
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RESULT 13
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 ; TOPOLOGY: 11; MOLECULE TYPE: US-08-175-155-48
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 Sequence 48, Appli-
Patent No. 5641648
 Query Match 33.4%; Score 1184.5; DB 1; Length Best Local Similarity 40.7%; Pred. No. 1.8e-78; Matches 272; Conservative 60; Mismatches 323; Indels
 GENERAL INFORMATION:
 TELEFAX: 415-398-3249 INFORMATION FOR SEQ ID NO:
 APPLICANT:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
 STREET: FOUL CITY: San Francisco
STATE: CA
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 APPLICANT: Dorman, Mary A.
TITLE OF INVENTION: Methods for Preparing Synthetic
TITLE OF INVENTION: Repetitive DNA
NUMBER OF SEQUENCES: 69
 REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hc
 ATTORNEY/AGENT INFORMATION:
 APPLICANT:
 SEQUENCE CHARACTERISTICS:
 666 YGPG 669
 725
 785 YGAG 788
 561 AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
 APPLICATION NUMBER: US/08/175,155
FILING DATE: 29-DEC-1993
CLASSIFICATION: 435
 NAME: Rowland, Bertram REGISTRATION NUMBER: 20
 ZIP: 94111
 COUNTRY:
 STRANDEDNESS: single
 LENGTH:
 7 GQQMGRGSMASGRGGLG-GQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGA 65
 GLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAG 244
 GSQGTSGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGPG-GYGPGQQTSGRG 184
 GAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGL 125
 GSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG---AGSG 560
 amino acid
 Application US/08175155
 E: Flehr, Hohbach, Test, Albritton & Herbert Four Embarcadero Center, Suite 3400
 1059 amino acids
 Cappello, Joseph
Crissman, John W.
 Ferrari, Franco A.
 linear
 peptide
 20015
 48:
 A-55186-5/BIR
 Length 1059;
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 Gaps
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RESULT 14
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 Sequence 54, App
Patent No. 58307
 GENERAL INFORMATION:
 APPLICANT:
APPLICANT:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
 APPLICATION NUMBER: US 08/053,049 FILING DATE: 22-APR-1993 PRIOR APPLICATION DATA:
 SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 1
 APPLICANT: DORMAN, MARY A.
TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
TITLE OF INVENTION: REPETITIVE DNA
 1035 AGAMDPGR 1042
 915
 543
 858
 484
 424
 798
 364
 189
 621
 738
 245
 APPLICATION NUMBER: US/08/707,237A FILING DATE: 03-SEP-1996 CLASSIFICATION: 435
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 STREET: Four Embarca
CITY: San Francisco
 STATE: California
 MEDIUM TYPE: Floppy disk
 COUNTRY: United States ZIP: 94111-4187
 ADDRESSEE:
 QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQG
 PGGYGPGQ 670
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 SQGTSGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAA 602
 GSGAGAGSGAGAGSGAGAGSGAG - - - AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
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 Application US/08707237A
 E: Flehr, Hohbach, Test, Albritton & Herbert Four Embarcadero Center, Suite 3400
 Crissman, John W.
 Capello, Joseph
09-NOV-1988
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 ; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-08-707-237A-54
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 Best Local Similarity
Matches 272; Conserv.
 Query Match
 INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1059 amino acids
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-CCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
 975 AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
 681
 424 GGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGA 483
 364 AAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGR
 305 AGAAAAAAAAAGGAGQGGYGGLGSQGTSGPG-GYGPGQQTSGRGGLGGQGAGAAAAAAA 363
 621 AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
 561 AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
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 66 GAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGL 125
 STRANDEDNESS:
 TELEFAX: (417, 77299 CFO ID
 TYPE: amino acid
 TELEPHONE:
 REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-10/WHD
 NAME: Trecartin, Richard F
 7 GQQMGRGSMASGRGGLG-GQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGA 65
PGGYGPGQ 670
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 AAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSG
 GSGAGAGSGAGAGSGAGAGSGAG----AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
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 Conservative 60; Mismatches
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 398-3249
 33.4%; Score 1184.5;
40.7%; Pred. No. 1.8
 54:
 .5; DB 2;
1.8e-78;
 323;
 Indels
 Length
 1059;
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503

443

1034

662 974 602 914 542 857 423

737

680 304 620 244 560 184

797

Gaps

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US-08-477-509B-83
; Sequence 83, Application US/08477509B
----nt No. 5770697
----nt No. 5770697
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 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-477-509B-83
 APPLIANCE APPLIANCE APPLIANCE APPLIANCE APPLIANCE OF A NOVELLA ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard F.

REGISTRATION NUMBER: 31,801

REFERENCE/DOCKET NUMBER: 3-55186-7/RFT/MTK

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

15-781-1989
 Query Match
Best Local Similarity
Matches 272; Conserv
 APPLICATION NUMBER: US 08/175,155
ETLING DATE: 29-DEC-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
ETLING DATE: 22-APR-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
ETLING DATE: 29-OCT-1987
 TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 83:
 APPLICANT: Ferrall, Joseph APPLICANT: Cappello, Joseph APPLICANT: Crissman, John w
 | ||:
1035 AGAMDPGR 1042
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
 APPLICANT: Dorman, Mary A
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
 SEQUENCE CHARACTERISTICS:
LENGTH: 1101 amino aci
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 PRIOR APPLICATION DATA:
 APPLICANT:
486
 426
 APPLICATION NUMBER: US/O FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
 CITY: San Francisco
STATE: California
 66
 TYPE: amino acid
STRANDEDNESS: si
 ZIP: 94111
 COUNTRY:
 STREET:
 ADDRESSEE:
 7
 GSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGA
 GOOMGRGSMASGRGGLG-GOGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGA 65
 E: Flehr, Hohbach, Test, Albritton & Herbert Four Embarcadero Center, Suite 3400
 1101 amino acids
 Conservative
 Floppy disk
 single
 33.4%;
 US/08/477,509B
 60;
 Score 1184.5; DB 1;
Pred. No. 1.9e-78;
0; Mismatches 323;
 Indels
 Length 1101;
 13;
 Gaps
 545
 485
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 Same
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 364 AAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGR 423
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 670
 1076
 1016
 899
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 542
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Search completed: July 3, 2001, 14:56:41 Job time: 531 sec This Page Blank (uspto)

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Result
No.
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Minimum DB
Maximum DB
 Title:
Perfect score:
 OM protein - protein search, using sw
 Database
 Total number of hits satisfying chosen parameters:
 Searched:
 Run on:
 Scoring table:
 Sequence:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1386
1281.5
1260.5
1242
1198.5
1196.5
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1032.5
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1014
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1007
999.9
988.5
977.5
977.5
977.5
979.933.5
 1138.5
1114.5
1110.5
 1180
1158.5
 Score
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 1152
1151
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length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
 BLOSUM62
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 US-09-490-291-6
3543
 July 3, 2001, 14:59:32; Search time 63.58 Seconds (without alignments) 827.880 Million cell updates/sec
 219241 segs, 76174552 residues
 1 MASMTGGQQMGRGSMASGRG.....TSGIRIRAPSTSFEHHHHHH
 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
 Length
 718
2639
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13079
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1538
1749
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883
7783
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7783
 DB
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F709612
F709635
E70895
D70835
D70835
C70974
A70807
G70917
F70620
F70620
F70620
A70893
 SUMMARIES
 model
 219241
 fibroin Chinese hypothetical glyci hypothetical glyci
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 Description
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GTA for residue

## ALIGNMENTS

						,-		· · ·			
Qy 393 AGAAAAAAAAAGGAGGGGGGGGGGGGGGGGGGGGG	Qy 351 GGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQG 392	QY 292 QGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGP-GQQTSGRGGL 350 	QY 253 SQGTSGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGS 291     :	Qy 202 AGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLG 252	Qy 142 GAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAA 201 	Qy 82 GGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAGGAGGGGGGGGGGGG	QY 25 QGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAG-AAAAAAAAAAAAAGGAGQ 81	Query Match 60.3%; Score 2138; DB 2; Length 718; Best Local Similarity 66.3%; Pred. No. 2e-113; Matches 498; Conservative 20; Mismatches 49; Indels 184; Gaps 35;	A;Status: preliminary A;Status: preliminary A;Molecule type: DNA A;Residues: 1-718 <xua> A;Cross-references: GB:M37137; NID:g159711; PID:g159712 A;Cross-references: GB:M37137; NID:g159711; PID:g159712 A;Note: the authors translated the codon GGT for residue 292 as Gln, GTA for residue</xua>	R;Xu, M.; Lewis, R.V. Proc. Natl. Acad. Sci. U.S.A. 87, 7120-7124, 1990 A;Title: Structure of a protein superfiber: spider dragline silk. A;Reference number: A36068; MUID:90384959 A:Acression: A36068	A36068 major ampullate fibroin protein - orb spider (Nephila clavipes) (fragment) C;Species: Nephila clavipes C;Date: 08-Mar-1991 #sequence_revision 13-Jan-1993 #text_change 09-Sep-1997 C;Accession: A36068

Qy 258 GRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRG 298 	Qy 2 ASMTGGQQMGRGSMASGRGGLGGQGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Query Match 39.1%; Score 1386; DB 2; Length 2639; Best Local Similarity 40.4%; Pred. No. 6.4e-71; Matches 412; Conservative 21; Mismatches 236; Indels 352; Gaps 40;	Db 371 AGAVAAAAGGAGGGGYGGLGSOGAGRCGGCAGAAAAAGGAGGAGGRGYGG 419  Qy 453 LGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Query Match 36.2%; Score 1281.5; DB 2; Length 1901; Best Local Similarity 39.5%; Pred. No. 3.6e-65; Matches 354; Conservative 28; Mismatches 273; Indels 241; Gaps 39;	RESULT 3 F70806 hypothetical glycine-rich protein Rv3508 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: F70806 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon C; Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rijandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987 A;Accession: F70806 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-1901 <col/> A;Cross-references: GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA17745.1; PID:g292 A;Experimental source: strain H37Rv C;Genetics: A;Gene: Rv3508 C;Superfamily: collagen alpha 1(IV) chain	Qy 688 H 688     Db 1587 H 1587	Qy       299 GLGG

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RESULT 4

Problet Result 4

Result 514 - Mycobacterium tuberculosis (strain Hopothetical glycine-rich protein Rv3514 - Mycobacterium tuberculosis (strain Hopothetical glycine-rich protein Strain Hopothetical glycine-rich protein Result 51 - Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 (c; Accession: D70807

R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Parkhill, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hopothetical glycine-result for Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
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 Holroyd,
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C;Genetics:
A;Gene: Rv3514
C;Superfamily: collagen alpha 1(IV) chain
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 Length
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 the complete
 Gaps
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 shown
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 PID: g292
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į	GARA GINGAGARAAR COMPONICATION
QY 336 GGYGPGQQTS(	451 GGLG
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A; Reference number: A70000; A; A; Accession: A70934 A; Status: preliminary; nuc A: Molecule type: DNA	A;Gene: Rv3512 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
jandream, M.A.; Ro ture 393, 537-544, Authors: Sqares, F Title: Deciphering	A;Residues: 1-1079 <col/> A;Residues: 1-1079 <col/> A;Residues: 1-1079 <col/> A;Cross-references: GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA17749.1; PID:g292444 A;Experimental source: strain H37Rv C;Genetics:
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n · · ⊢ · 0	A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987
RESULT 6	R;COLE, S.T.; BrOSCN, K.; PARKNIII, J.; GATRIER, T.; CRUTCHER, C.; RALLIS, D.; GOLDON, S.; CONNOT, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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Qy 506 QQTSGRGGLGGQGAGA                   Db 646 GANGGAGGAGGSGGGT	Qy 632GAGAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYG 667     :
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 ulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
biology of Mycobacterium tuberculosis from the complete
00; MUID:98295987
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 IGGSGSDGVNGSSAGADGHPGGTGGVGGTGGKGGDGGDGGAAPNGV 756
 ılpha 1(IV) chain
 cleic acid sequence not shown; translation not shown
 protein Rv0578c - Mycobacterium tuberculosis (strain H37RV) tuberculosis
 Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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A; Residues: 1-1381 <COL>
A; Residues: 1-1381 <COL>
A; Cross-references: GB: AL022022; GB: AL123456;
A; Experimental source: strain H37Rv
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 A:Gene: Rv3507
C:Superfamily: collagen alpha 1(IV) chain
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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 Query Match
Best Local S
Matches 319
 1053
 150
 326
 210
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es 319; Conserv
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 SG 674
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366
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 269
 1168
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 641 AAAAGGAG-OGGYGGLGSQGTSGPGGYGPGQQTSGIRIRAPSTS 683
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RESULT E

C; Genetics: A; Gene: Rv2490c C; Superfamily: Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.;
A; Title: Deciphering the biology of Mycobacterium
A; Reference number: A70500; MUID:98295987
A; Accession: A70869 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 hypothetical glycine-rich protein Rv2490c - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: A70869 A; Molecule type: DNA A; Residues: 1-1660 <COL> A; Experimental A;Cross-references: GB:AL021246; A;Experimental source: strain H3 A; Status: preliminary; nucleic acid sequence Rv2490c collagen alpha 1(IV) chain GB:AL123456; NID:g3261507; PIDN:CAA16067.1; PID:g279 7Rv not shown; translation not Whitehead, S.; Barrell, B.G. tuberculosis from the complete Holroyd, H37RV) genc

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Query Match Best Local S Matches 326

Local Similarity 37.0 nes 326; Conservative

33.3%;

Score 1180; D Pred. No. 1.6e 38; Mismatches

DB 2; L.6e-59; nes 292;

Length 1660; Indels 212

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Gaps

35;

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A; Accession: H70846
A; Status: preliminary; nucleic acid sequence not shown; translatials; Molecule type: DNA
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C;Genetics:
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C;Superfamily: collagen alpha 1(IV) chain
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 GAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGA---------
 GNGGNGGIGGNGGSAAGTGGDGGKGGNGGAGANGQDFSASANGANGGQGGNGGNGGIGGK
 GLGGQGA-GAAAAAAAAAGGAGQGGYGGLGSQ------GTSGRGGLGGQ 101
 GTAPTSGGNGGAGATPTVAGENGGAGGNGGHGGSVGNGGAGGAGGNGVAGTGLALNG
 GRGSMASGRGGIGGQGAGAAAAAAAAAAAAAGG------AGQGGYGGIGSQGTSG-----RG
 G--GNVGLGGDAGSGGAGGNGGIGTDAGGAGGAGGAGGNGGSSKSTTTGNAGSGGAGGNG
 -----AGQGGYGGLGSQGTSGRGGLGSQGAGAAAAAAAAAAGGAGQGGYGGLGSQ 494
 GGNGGKGGTAGNGSGAAGGNGGNGGSGLNGGDAGNGGNGGALNQAGFFGTGGKGGNGGN
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 GGNGGNGASPTVAGGNGGDGGKGGSGGNVGNGGNGGAGGNGAAGQAGTPGPTSGDSGTSG
 GGDAFATFAKAGNGGAGGNG----GNVGVAGQGGAGGKGAIPAMKGATGADGTAPTSGGD
 ASGSGYVNYTAGHGGNGGNGGNGSAGAGGQGGAGGSAGNGGHGGGATGGDGGNGGNG 1382
 AAAA-----AAAAGGAGQGGYGGLGSQGTSGRGGL-----GGQGAGAAA-----
 GTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAAGG-----AGQGGYGGLG
 GVSETGFGGAGGNGGYGGPG--GPEGNGGLGGNGGAGGNGGVSTTGGDGGAGGKGGNGGD
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 Similarity
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 32.7%;
 34;
 Score 1158.5; DB 2; Pred. No. 2.4e-58;
 Mismatches
 305; Indels
 Length
 247;
 674
 Gaps
 542
 1204
 1146
 1262
 444
 906
 850
 246
 188
 676
 616
 792
 141
 303
 288
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RESULT 10

270917

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hypothetical glycine-rich protein Rv1450c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: E70917
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genor A;Accession: E70917
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Respeciales: 1-1329 <COL>
A;Cross-references: GB:295844; GB:AL123456; NID:g3250713; PIDN:CAB09271.1; PID:g21310.
A;Experimental source: strain H37RV
A;Experimental source: strain H37RV
 C:Genetics:
A:Gene: Rv1450c
C:Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology
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Matches 326; Conserv
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 197
 102
 193
 133
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 -GQGGYGGLGSQGT-----SGPGGYGPGQQTSGRGGLGGQGA------
 Conservative
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 Length 1329
 Indels 244;
 PIDN:CAB09271.1; PID:g2131046
 Gaps
 196
 669
 429
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 H37RV)
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RESULT 11
A70896
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A70896
C;Decies: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Decies: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 24-Nov-1999
C;Accession: A70896
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr: Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Recession: A70896
A;Reference number: A70500; MUID:98295987
A;Accession: A70896
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA, A; Residues: 1-853 <CDL>
A; Cross references: GB.AL021897; GB:AL123456; NID:g3256022; A; Experimental source: strain H37Rv C; Genetics: A; Gene: Rv1091 C; Superfamily: unassigned collagens
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 Query Match
Best Local Similarity
 Matches
 1022 ---PAGSILH 1028
 311
 677 IRAPSTSFEH
 790 NPGAGGQGGSGGAGSTPGAKGAHGFTPTSGGDGGDGGNGGN-----SQVVGGNGGDGGNG
 7
 GQGGYGGLG--SQGTSGPGGYGPGQQTS----GRGGLGGQGA----GAAAAAAAAAAGGA 205
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 AGGAAGLFGDAGAGGNGGKGGAGGAAFSINFTAGDGGAGGAGGSGGHALLWGAGGAGGNG
 GAAAAAAAAAAGGAGQGGYGGLG-----SQGTSGRGGLGGQGAGAAAAAAAAAAAGGA 155
 YGNGGAGGAGGTSVIPGVAGGNGGAGGSAGLWGTGGAGGDGGNGRSGPVNVAGSAGGNGG
 -GRGGLGGQGAGAAAAAAAAAGGA-----GQGGYGGLGSQGTSG----RGGLGGQGA 103
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 301;
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 Conservative
 32.5%;
 ; Score 1151; DB 2;
; Pred. No. 4.1e-58;
27; Mismatches 307;
 -----SQGTSGR 625
 Length 853;
 Indels 110;
 PIDN:CAA17207.1;
 Gaps
 370
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 28;
 Holroyd,
 PID:e125
 H37RV)
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R;Hinman, M.B.; Lewis, R.V.

J. Biol. Chem. 267, 19320-19324, 1992
A;Title: Isolation of a clone encoding a second dragline silk file.
A;Reference number: A44112; MUID:92406876
A;Accession: A44112
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-627 <HIN>
A;Cross-references: GB:M92913; NID:g159713; PID:g159714
A;Cross-reference extracted from NCBI backbone (NCBIP:l13893)
R;Hinman, M.B.; Lewis, R.V.
submitted to the EMBL Data Library, May 1992
A;Description: Isolation of a clone encoding a second dragline shapescription: Isolation of a clone encoding a second dragline shapescription: Isolation of a clone encoding a second dragline shapescription: Isolation of a clone encoding a second dragline shapescription: Isolation of a clone encoding a second dragline shapescription: Isolation of a clone encoding a second dragline shapescription: Isolation of a clone encoding a second dragline shapescription: S27824
A;Residues: 19-627 <HIZ>
A;Cross-references: EMBL:M92913
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 N;Alternate names: silk fibroin, dragline
C;Speckes: Nephila clavipes
C;Date: 31-Dec_1993 #sequence_revision 31-Dec-1993
C;Accession: A44112; S27824
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 Query Match 32.1%; Score 1138.5; DB 2; Best Local Similarity 47.0%; Pred. No. 1.6e-57; Matches 325; Conservative 36; Mismatches 190;
 471
 485
 819
 713
 651 GYGGLGSQGTSGPGGYGPGQQTSGI 675
 102
 134
 43
 23
 79
 12
 N
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 PGQQGPGGYGPGQQGPGRYGPGQQGPSGPGSAAAAAA-GSGQQGPGGYGPRQQGPGGYGQ 101
-GQGAGAAAAAAAAGGAGQGGYGGLGSQGTSGRG----GLGGQGAGAAAAAAAAAAAGG
 dragline silk fibroin - orb spider (Nephila clavipes) (fragment)
 May 1992 encoding a second dragline silk fibroin: Nephila cla
 #text_change
 Indels 141;
 Length
 silk fibroin. Nephila clavipes
 20-Mar-1998
 Gaps
 530
 539
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 242
 187
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 GGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSG--RGGLGGQGAG
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 QGPGGYG----PGQQGPGGYGPGQQGLSGPGSAAAAAAAAGPGQQGPGGYGP-GQQGPSGP
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 587
 463
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 272
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R:COle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987

A;Accession: A70812
A;Status: preliminary; nucleic acid sequence not shown; translation not shown RESULT 13
A70812
bypothetical glycine-rich protein Rv0833 - Mycobacterium tuberculosis (strain hypothetical glycine-rich protein Rv0833 - Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis
C;Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: A70812 Q 밁 δã QY A; Gene: Rv0833 C; Superfamily: A; Molecule type: DNA A; Residues: 1-749 <COL> A; Cross-references: GB: 밁 A;Cross-references: GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAA17639.1; PID:g291 A;Experimental source: strain H37Rv Best Loc Matches Genetics: Query Match 18 Local GRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQ---GGLGGQGAGAAAAAAAAAAGGA------GQGGYGGLGSQGTSGRGGLGGQGAGAAAAAA 110 GNGGAGGSGAPGAIGGAGGPAGLIGVGGAGGAGGAGGAAGGAGGAALLFGAGGA 62 GGAGGSG-GSGAAGGAGGAGGLFASGGSGGFGGFASTGTGGAGGTGGAGGLFASGGV 121 303; Similarity elastin Conservative 31.5%; Score 1114.5; DB 2; 39.6%; Pred. No. 4.1e-56; tive 18; Mismatches 309; Indels Length 749; -----GTSGR 57 135; Gaps 32; Holroyd, H37RV) geno

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hypothetical glycine-rich protein Rv1759c - Mycobacterium tuberculosis (strain H37R N; Alternate names: wag22 antigen homolog C; Species: Mycobacterium tuberculosis C; Species: Mycobacterium tuberculosis C; Species: N; Gyobacterium tuberculosis C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C; Accession: H70987 R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gord; Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroy Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete ge A; Reference number: A70500; MUID:98295987 A; Recession: H70987 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-914 <COL> A; Cross-references: GB:295890; GB:AL123456; NID:93242245; PIDN:CAB09322.1; PID:9213 A; Experimental source: strain H37Rv C; Superfamily: elastin H37Rv C; Superfamily: elastin
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 Query Match 31.3%; Score 1110.5; DB 2 Best Local Similarity 38.2%; Pred. No. 7.9e-56; Matches 309; Conservative 31; Mismatches 307;
 632
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 -----AAAAAAAAAAAGGAGQGGYGGLGSQ----GTSGRGGLGGQGAGAAAAAAAAAA 316
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 Length
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 Gaps
 697
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 179
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 Holroyd,
 Gordon,
 H37RV)
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 ---QGTSGRGGLGGQG--AGAAAAAAAAAGGAGQGGYGGLGSQG--TSGRGGLGGQGAG
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 -AGOGGYGGLGSOGT---SGRGGLGGOGAGAAAAAAAAAAAAGGAG-----OGGYGGLGS--
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 -AGQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAGG------
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 487
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 525
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hypothetical glycine-rich protein Rv0834c - Mycobacterium tuberculosis (strain c;Specles: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: B70812
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devili, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
R,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Reference number: A70500; MUID:98295987
A; Reference number: A70500; MUID:98295987
A; Molecule type: DNA
A; Residues: 1-882 <COL> RESULT B70812 complete Holroyd,

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A;Cross-references: GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAA17640.1; PID:g291689
A;Experimental source: strain H37Rv
C;GenetLcs:
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 176 -PGQQTSGRGGLGGQGAGAAAAAAAAAAAGGAG------QGGYGGLGSQGTSGRG 222
 191 LWGSGGAGGAGGSG-GGSGGAGGNALMFGIGGNGGAGGAASGVGNGGVGGAGGAGGALVA 249
 133 GEAGGPGGWLLGNGGNGGSGAPGQTGGAGGAAGLLGHGGTGGAG--GTGASGGKGGTGGW 190
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 309 SPFGIDIGIGGAGGHG-GAGTNGGAGGAGGAGGSSGTVFALDLSWGGAGGNGGAATTGTG
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 643 AAGGAGQG-----
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39.7%; Pred. No. 2.7e-54;
ative 28; Mismatches 306; Indels 130; Gaps
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Search completed: July Job time: 365 sec

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678:56:660
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is derived by analysis of the total score distribution.
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3543
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 93435 seqs, 34255486 residues
 GenCore version Copyright (c) 1993 - 2000
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CAFF_RIFPA
GRP_ARATH
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YI40_MYCTU
CA13_HUMAN
YK98_MYCTU
CA13_HOUSE
CA13_BOVIN
YA68_MYCTU
CA13_BOVIN
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 "Sequence conservation in the C-terminal region of spider silk proteins (Spidroin) from Nephila clavipes (Tetragnathidae) and Araneus bicentenarius (Araneidae).";
J. Biol. Cham. 269:6661-6663(1994).
-i- FUNCTION: THIS SPIDER MAJOR AMPULLATE SILK POSSESSES UNIQUE CHARACTERISTICS OF STRENGTH AND ELASTICITY. IT MAY CONSIST OF PSEUDOCRISTALLINE REGIONS OF ANTIPARALLEL BETA-SHEET INTERSPERSED WITH ELASTIC AMORPHOUS SEGMENTS.
-i- SUBUNIT: MAJOR SUBUNIT, WITH SPIDROIN 2, OF THE DRAGLINE SILK.
-i- SUBCELLULAR LOCATION: EXTRACELLULAR.
 SPD1_NEPCL STANDARD; PRT; 747 AA. P.19837; P.19837; O1-FEB-1991 (Rel. 17, Created) O1-NOV-1995 (Rel. 32, Last sequence update) O1-OCT-1996 (Rel. 34, Last annotation update) SPIDROIN 1 (PRAGMENT).
 Nephila clavipes (Orb spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila.
 PIR; A36068; A36068.
Silk; Repeat.
 EMBL; M37137; AAA29380.1; -. EMBL; U03848; AAB60212.1; -.
 MEDLINE=94165058; PubMed=8120021;
Beckwitt R., Arcidiacono S.;
 SEQUENCE OF 653-747 FROM N.A.
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE=90384959; PubMed=2402494;
REPEAT
 "Structure of a protein superfiber: spider dragline silk.";
Proc. Natl. Acad. Sci. U.S.A. 87:7120-7124(1990).
 Xu M., Lewis R.V.;
 NCBI_TaxID=6915;
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 498;
 Similarity
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Pred. No. 3.2e<sup>-</sup>
20; Mismatches
 (IN REF. 1).
850E44B0D649E012 CRC64;
 NPGLSGCDVLIQALLEVVSALIQILGSSSIGQVNYGSAGQA
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(IN REF. 1)
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV3508 PRECURSOR.
RV3508 OR MTV023.15.
 Hypothetical protein; Repeat; SIGNAL 1 30 1
 InterPro; IPR000084; -. Pfam; PF00934; PE; 1.
 Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;
 SEQUENCE
 HSSP; P19972; 1KVD.
TubercuList; Rv3508; -.
 EMBL; AL022022; CAA17745.1; -.
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 Actinomycetales;
 SEQUENCE FROM N.A.
 588
 340
 91
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 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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28; Mismatches
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 Length
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 FIBH.
 Yang T
 Zhou
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glo: Bombycoldea; Bombycoldee; Bombyx.
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 FIBROIN HEAVY
 1054
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 C.-Z., Confalonieri F., Medina N., Zi
T., Jacquet M., Janin J., Duguet M.,
Jerianization of Bombyx mori filbroin
eic Acids Res. 28:2413-2419(2000).
 NFNGCQGGAGGQGGCQGGLGGASTTSINANGGAGGNGGTGGKGGAGGAGTLGVGGSG
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Tanaka K., Kajiyama N., Ishikura K., Waga S., Kikuchi A., Ohtomo K., A Takagi T., Mizuno S.;

A Dischim. Biophys. Acta 1432:92-103(1999).

Biochim. Biophys. Acta 1432:92-103(1999).

C INSOLUBLE AND CHEMICALLY INERT FIBRE.

C INSOLUBLE SPECIFICITY: PRODUCED EXCLUSIVELY IN THE POSTERIOR (PSG)

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C SECTION OF SILK CLANDS.

C IDMAIN: COMPOSED OF ANTIPARALLEL BETA SHEETS. THE STRANDS OF THE BETA SHEETS COMPOSED OF MICROCRYSTALLINE ARRAYS OF (-GLY-SER-GLY-ALA-)N INTERRUPTED BY REGIONS CONTAINING BULKLER RESIDUES.

THE FIBER IS COMPOSED OF MICROCRYSTALLINE ARRAYS ALTERNATING WITH
 PARTIAL SEQUENCE FROM N.A. MEDLINE-94365842; PubMed-7916056; MAIA K., Ichimura S., James T.C.; "Highly repetitive structure and gene.";
 MEDLINE-89094868; PubMed-3210244; Mita K., Ichimura S., Zama M., James "Specific codon usage pattern and its structure of silk fibroin mRNA."; J. Mol. Biol. 203:917-925(1988).
 gene.";
J. Mol. Evol. 38:583-592(1994).
 Tsujimoto Y., Suzuki Y.;
"Structural analysis of the surrounding regions.";
Cell 16:425-436(1979).
 SEQUENCE OF 1-168 FROM N.A.
MEDLINE-80045039; PubMed-498286;
Tsujimoto Y., Suzuki Y.;
"The DNA sequence of Bombyx mori
 MEDLINE-99296390; PubMed-10366732;
 STRAIN-J-139;
 SEQUENCE OF 5179-5263
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 PARTIAL SEQUENCE FROM N.A. MEDLINE-79211211; PubMed-455439;
 Cell 18:591-600(1979).
 "The DNA sequence of Bombyx mori fibroin gene flanking, mRNA coding, entire intervening and
 AMORPHOUS REGIONS.
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L; V00094; CAA32432.1; -.
L; V00097; CAA32433.1; -.
L; S74439; AAB31861.1; -.
L; X1386; CAA32076.1; -.
L; AB3186; CAA32076.1; -.
L; AB017362; BAA33147.1; -. S01844; S01844. Signal; Repeat 22 149 5244 POTENTIAL.
FIBROIN HEAVY CHAIN.
HIGHLY REPETITIVE.
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 AAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAAAGGAGQG-GYG-GLGSQGTSG
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 AGAGSGAASGAGAGAGTGSSG
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 STANDARD;
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1A; 391586
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 -GYG-GLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQG---GYG
 33.1%;
 Created)
 Last sequence up
 49;
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 Score 1174.5; DB
Pred. No. 1.7e-45;
9; Mismatches 305
 5138
 674
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 V (IN REF. 2).
8EE11D3AOA47440E CRC64;
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 Indels
 Length
 131;
 Gaps
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 EMBL;
 REPEAT
 REPEAT
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 134
 43
 79
 23
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Hinman M.B., Lewis R.V.;

"Isolation of a clone encoding a second dragline silk fibroin.

Nephila clavipes dragline silk is a two-protein fiber.";

J. Biol. Chem. 267:19320-19324(1992).

-I- FUNCTION: THIS SPIDER MAJOR AMPULLATE SILK POSSESSES UNIQUE CHARACTERISTICS OF STRENGTH AND ELASTICITY. IT MAY CONSIST C PSBUDGCRISTALLINE REGIONS OF ANTIPARALLEL BETA-SHEET INTERSE WITH ELASTIC AMORPHOUS SEGMENTS.

WITH ELASTIC AMORPHOUS SEGMENTS.
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 SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
Nephila clavipes (Orb spider).
Eukaryota, Metazoa, Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
 MEDLINE-92406876; PubMed-1527052;
 SEQUENCE FROM N.A.
 SUBCELLULAR LOCATION: EXTRACELLULAR.
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 Conservative
 32.1%;
 54184
 MW;
 Score 1138.5;
Pred. No. 2e-4
36; Mismatches
 36;
 CB9B63779B2C594B CRC64;
 APPROXIMATE TANDEM REPEATS
 DB 1;
 190;
 OF THE DRAGLINE SILK
 Indels 141;
 Length
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 MEDLINE-98295987; PubMed-9634230;

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Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,

MacCole S.T., Brosch R., Gas S., Barry C.E. III, Tekala F.,

MacCole S., Basham D., Brown D., Chillingworth T., Connor R.,

MacCole S., Hamlin N., Holroyd S.,

MacLean J., Moule S., Hamlin N., Holroyd S.,

MacLean J., Moule S., Murphy L.,

MacLean J., Moule J., Moule S., Murphy L.,

MacLean J., Moule J., Moule J., Moule J.,

MacLean J., Moule J., Moule J., Moule
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WA22_MYCTU
006794;
30-MAY-2000
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 SEQUENCE FROM N.A. STRAIN-H37RV;
 EMBL; 295890;
HSSP; P41140;
 Actinomycetales;
NCBI_TaxID-1773;
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
 Mycobacterium tuberculosis.
 WAG22 ANTIGEN PRECURSOR. WAG22 OR RV1759C OR MTCY
 TubercuList; Rv1759c; -.
 30-MAY-2000 (Rel. 39, Last sequence up 30-MAY-2000 (Rel. 39, Last annotation
 556
 501
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 464
 531
 418
 471
 370
 413
 311
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 273
 298
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 (Rel. 39, Created)
 CAB09322.1;
 STANDARD;
 OR MTCY28.25C.
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RESULT 6
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 874 GNAVVIGNGGNGGNAGKAGGTAGAGGAG
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 5 TGGQQMGRGSMASGRGGLGGQGAGAAAAAAAAAAGGAG----QGGYGGL-GSQGTSGRGG
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 31
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 31.38;
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 667
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 CRC64;
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 544
 694
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 432
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AMEDLINE-9829987; PubMed-9634230;
ACOLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
AGORDON S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
AGORDON S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
AGORDON S.V., Eaglam D., Brown D., Chillingworth T., Connor R.,
AGORDON S., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
AGOLIVER S., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
AGOLIVER S., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
AGOLIVER S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
AGORDON S., Segures S., Segures J.,
AGORDON S., Segures S., Squares R., Sulston J.E.
AGORDON S., Whitehead S., Barrell B.G.;
AGORDON S., WHITEHEAM S., WARRELL, PERMILY; PGRS
AGORDON S., WARRELL, PERMILY, PGRS
AGORDON S., WARRELL, PROMILY, PGRS
AGORDON S., WARRELL, PROMILY,
 Query Match
Best Local
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TubercuList; Rv2634c; -.
InterPro; IPR001899; -.
InterPro; IPR001899; -.
Pfam; PF00934; PE; 1.
 01-NOV-1997 (Rel. 35, 1
30-MAY-2000 (Rel. 39, 1
HYPOTHETICAL PE-PGRS FJ
RV2634C OR MTCY441.04C
 Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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 SEQUENCE FROM N.A.
 NCBI_TaxID:1773;
 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
 Hypothetical protein SEQUENCE 778 AA;
 entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 244
 129
 58
 send an email to license@isb-sib.ch).
 7
 SUBFAMILY.
 GQQMGRGSMASGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQ------GTSGR
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 Similarity
 Conservative
 , Last sequence update)
, Last annotation update)
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 63131 MW;
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 Score 1049.5; DB 1; Length Pred. No. 1.8e-40;
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 Indels
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 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Oliver S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.; Taylor K., Whitehead S., Barrell B.G.; Roceiphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
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 Y278_MYCTU STANDARD; PRT; 957 AA. p56877; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) HYPOTHETICAL PE-PORS FAMILY PROTEIN RV0278C PRV0278C OR MTV035.06C.
 MYCTU
 MEDLINE-98295987; PubMed-9634230;
 SEQUENCE FROM N.A.
 InterPro; IPR000084;
Pfam; PF00934; PE; 1
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 461
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 456
 Hypothetical protein;
 TubercuList; Rv0278c; -.
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 AGGVGGAGGEGLTDGAGTAEGGT--GGLGGLG--GVGGTGGMG-----GSGGVGGNGGA
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 -GTGGTGGAGGTTGGSGGAGGLIGWAGAAGGTGAGGTGGQGGLGGQG--GNGGNGGT
 BELONGS
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 TO THE MYCOBACTERIAL
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 PΕ
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 671
 Mycobacterium
 PGRS
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71EBABD417FBA47C CRC64;

30 957 81905

> POTENTIAL. HYPOTHETICAL RV0278C

PE-PGRS FAMILY PROTEIN

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RESULT 8
Y747_MYCTU STANDARD; PRT; 801
ID Y747_MYCTU STANDARD; PRT; 801
AC 053810;
DT 30-MAY-2000 (Rel. 39, Last sequence upda
DT 30-MAY-2000 (Rel. 39, Last sequence upda
DT 30-MAY-2000 (Rel. 39, Last annotation up-
DE HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV07.
GN MYCODBacterium tuberculosis.
OC Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Act
OC Actinomycetales; Corynebacterineae; Mycol
OX NCBLTaxID-1773;
RN [1]
RP SEQUENCE FROM N.A.
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 186
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 29.18;
 29;
 Score 1032; DB 1;
Pred. No. 1.2e-39;
 Mismatches 313;
 on update)
RV0747 PRECURSOR
 update)
 Mycobacteriaceae;
 801
 Actinobacteridae;
 -GAGTGGTGGDGGHAGVFGNGGDG
 Length
 Indels 146;
 Mycobacterium
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Matches 277
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harri Gordon S.V., Eiglmeker K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
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 Pfam; PF00934; PE; 1.

Pfam; PF00934; PE; 1.

SIGNAL 1 30 F
31 801
 SEQUENCE
 InterPro; IPR000084; Pfam; PF00934; PE; 1
 TubercuList; Rv0747;
 EMBL; AL021958; CAA17514.1; -.
 MEDLINE=98295987; PubMed=9634230;
 427
 461
 404
 129
 Local Similarity
 71
 11
 SUBFAMILY.
 SIMILARITY: BELONGS
 GGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQG
 GGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGG----AGQGGYGGLGSQ-GTSGRGGL
 GGTGGSGGPGATGLGGIGGAGGAALLFGSGGAGGSGGAGAVGGNGGAGGNAGALLGAAGA
 AGQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGA-----GAAAAAAAAAAGGAGQ
 GRPLIGNGANGTPGTGADGGAGGWLFGNGGNGGQGTI--GGVNG-GAGGAGGAGGILFGT
 -----GAAAAAAAAAAGGAGQG--GYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGG
 GNGGSGGTGA--TLGKAGIGGTGGVLLGLDGFTAPASTSPLHTLQQDVINMVNDPFQTLT
 GQGGYGGLGSQGTSGRGGLGGQGA-----
 GGAG-GISKSYGDSAAGGAG-GAPGLIGNGGNGGNGGASTGGGDGGPGGAGGTGYLIGNG
 GGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGL---GGQGAGAAAAAAAAAAAAGGA
 GSGGSGNLTGGAGGAGGNAGTLATGDGGAGGTGGASRSGGFGGAGGAGGDAGMFFGSGGS
 GTSGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLG-SQGTSGPGGY-GPGQQTSGRGGL 186
 STDVAGGAGGAGGAGGAGMLFGAAGVGGVGGFSNG-GATGGAGGAGGAGGAG-GLFGAGRER
 AAAAAAAGGAGQGGYGGLGSQ--GTSGRGGLGGQGAGAAAAAAAAAAAAAAGGAGQGGYGGLGSQ
 GRPLIGNGANGAPGTGANGGPGGWLIGNGGAGGSGAPGAGAGGNGGAGGLFGSG-GAGGA
 801
 Conservative
 AA;
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801
 65407 MW;
 27.9%;
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 TO THE MYCOBACTERIAL
 -GLFANGGAGGPGGFGSPAGAGGIGGAGGNGGLFGAGGT
 Score 988.5;
Pred. No. 8.5
 HYPOTHETICAL RV0747.
 POTENTIAL
 Signal
 EA54C9BF45A00F41 CRC64;
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01-OCT-1996 (Rel. 3
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 MEDLINE-95130069; PubMed-7829060; Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.; "Use of an intron polymorphism to localize the tropoelastin mouse chromosome 5 in a region of linkage conservation with chromosome 7.";
 CHAIN
 Genomics 23:125-131(1994).

11- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS A NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER
-1- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 SEQUENCE
 SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Lung;
 Mus musculus (Mouse)
 ELASTIN PRECURSOR (TROPOELASTIN).
 MGD; MGI:95317;
 NCBI_TaxID-10090;
 796
 738
 487
 13
 78
 INTO AN EXTENSIBLE 3D NETWORK.
SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS
 PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
 GLNG
 AAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAA-AAAAAAAAAGGAGQGGYGG--LGSQ
 GTSG
 GGAGGAGGDAGLLVGSGGAGGAGASAT-GAATGGDGGAG--GKSGAFGLGGDGGAGGATG
 SGRGGLGGQ-----GAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAA
 GDAGLLSLGASGGAGGSGGSSLTAAGVVGGIG-----GAGGLLFGSGGAGGSGGFSNSGN
 GYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGT
 GTFGAGPGGLGGAGPGAGLGAFPAGTFPGAGALVPGGAAGAAAAYKAAAKAGAGLGGVGG
 GSMASGRGGLGGQG-----
 LSGAFHIGGKGGVG--GSAVLIGNGGNGGNGGNSGNAGKSGGAPGPSGAGGAGGLLLGEN
 GGAGGGSTLAGGAGGAGGNG---
 U08210; AAA80155.1;
 P04002; 1WFA.
 799
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 28
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 protein;
 Conservative
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 STANDARD;
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 34, Created)34, Last sequence up34, Last annotation
 860
71955
 Repeat;
 Chordata;
Rodentia;
 27.5%;
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 36;
 Signal; Con
POTENTIAL.
 Score 976; DB 1; Pred. No. 3.1e-37;
 ELASTIN
 Craniata; Vertebrata; I
Sciurognathi; Muridae;
 PRT;
 OCOBE5AAE1EDD7F1
 -----AGAAAAAAAAAGGAGQGGYGG
 Mismatches
 --GLFGAGGTGGAGSHSTAAGVSGGAGGA--G
 Connective
 update)
 860
 update)
 ξ
 tissue.
 Length 860;
 CRC64
 Indels
 Euteleostomi;
 Murinae;
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ED TOGETHER
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Q99372;
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01-OCT-1996 (
01-OCT-2000 (
 RAT
 SEQUENCE FROM N.A.

MEDLINE-91104868; PubMed-1702999;

Pierce R.A., Deak S.B., Stolle C.A., Boy

"Heterogeneity of rat troppelastin mRNA
Biochemistry 29:9677-9683(1990).
 ELASTIN
ELN.
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
Biochemistry
[2]
 NCBI_TaxID=10116;
 649
 545
 811
 632
 754
 703
 479
 589
 430
 485
 322
 425
 269
 365
 238
 305
 190
 245
 152
 185
 108
 138
 49
 10
 GFGLSPIYPGGGAGGLGVGGKPPKPYGGALGALGYQGGGCFG
 GAGAAAAAAAAAAGGAGQGG-----YGG-LGSQGTSGPGGYG
 GLGAGGLGAGGL-GAGGLGAGGGVSPAAAAKAAKYGAAGLGGV--LGARPFPGGGVAARP
 GY--GGLGSQGTSGRGGLG-GQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQ
 GRVAGAAPPAAAAAAAKAAAKAAQYGLGGAGGLGAGGLGAGGLG
 ---AGAA-AAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQG
 GAGVPGFGAGAVPGSLAASKAAKYGAAGGLGGPGGLGGPGGLG-----GPGGLGGAGVP
 AAG----GAG-------QGGYGGLGSQ-GTSGPGGYGPGQQTSGRGGLGGQG--
 GAGAAAAAAA-----AAAG-GAGQGGYG-GLGSQGTSGRGGLGGQGAGAAAAAAAA
 QGGY-GGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQ
 GGYGGLGSQGTSGPG---GYGPG--QQTSGRGGLGGQGAGAAAAAAAAA-----AG-GAG
 SPAAAAKAAKKAAKYGARGGVGIPTYGVGAGGFPGYGVGAGAGLGGASPAAAAAAAKAAK
 AAAAAAAAAAAAGGA----GQGGYG----GLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQ
 GTGVGSQAAAAAAKAAKYGAGGAGVLPGVGGGGIPGGAGAIPGIGGIAGAGTPAAAAAAK
 GGGAFSGIPGVGPFGGQQPGVPLGYPIKAPKLPGGYGLPYTNGKLPYGVAGAGGKAGYPT
 VVPQVGAGIGAGGKPGKVPGVGLPGVYPGGVLPGTGARFPGVGVLPGVPTGTGVKAKAPG
 V--PGGVGVGGVPGGVGVGVG----GVPGGVGVGGVPG----GVGGIGGIGGIGGXSTGA
 LGSQGTSGRGGL-GGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAA
 GSPAAAKSAAKAAAKAQYRAAAGLGAGVPGFGAGAGVPGFGAGAGVPGFGA
 VGGVPGGVGVGGIPGGVGVGG-----
 YGAGGAGALGGLVPGAVPGALPGAVPAVPGAGGVPGAGTPAAAAAAAAAKAAKAGLGPG
 AAAKAAKYGAAGGLVPGGPGVRLPGAGIPGVGGIPGVGGIPGVGGPGIGGPGIVGGPGAV
 AAAGGA-----GQGGYGGLGSQGTSGRGGLGGQGAG
 AGGAGOG--GYGGLGSO-----GTSGPGGYG----PGQQTSGRGGLGGQ----
 AAAAAAAG-GAG--QGGYGGLGSQGTSGRGGLGGQGA-----GAAAAAAAAA
 (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
CURSOR (TROPOELASTIN) (FRAGMENT).
 STANDARD;
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
 PRT;
 -----VPGGVGPGGVTGIG----AGPGGLGGA
 Boyd C.D.;
RNA revealed
 864
 B
 667
 852
 γď
 cDNA cloning.";
 AGGLGAG
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Rattus

810

631 753 648 478 588 429

702

370 484 424

321

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268

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 Query Match
Best Local Similarity
 EMBL; M60647; AAA42269.1; -.
EMBL; M60372; AAA42271.1; -.
EMBL; M86372; AAA42271.1; JOINED.
EMBL; M86355; AAA42271.1; JOINED.
EMBL; M86363; AAA42271.1; JOINED.
EMBL; M86364; AAA42271.1; JOINED.
EMBL; M86364; AAA42271.1; JOINED.
EMBL; M86371; AAA42271.1; JOINED.
EMBL; M86371; AAA42271.1; JOINED.
EMBL; M86373; AAA42272.1; JOINED.
EMBL; M86375; AAA42272.1; JOINED.
 J. Biol.
[3]
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 Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.;
"Elements of the rat tropoelastin gene associated with alternative splicing.";
Genomics 12:651-658(1992).
 or send an
 -
 SEQUENCE OF 781-864 FROM N. MEDLINE-88330868; PubMed-29
 VARIANT
 Alternative
 MEDLINE=92241859; PubMed=1572637
 SEQUENCE OF 264-533 AND 558-864 FROM N.A
 Deak S.B., Plerce R.A., Belsky S.A., Riley D.J., Boyd C.D.; "Rat tropoelastin is synthesized from a 3.5-kilobase mRNA."; Biol. Chem. 263:13504-13507(1988).
 191
 112
 113
 69
 53
 20
 FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS NUCHAL LICAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKEL INTO AN EXTENSIBLE 3D NETWORK.
SUBGELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC ALTERNATIVE PRODUCTS: THREE DIFFERENT MRNAS HAVE BEEN ARE PRODUCED BY ALTERNATIVE SPLICING.

PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
 AAAG-GAG--QGGYGGLGSQGTSGRGGLGGQGA------GAAAAAAAAAAAAAGGA 155
 GGLGGQGAGAAAAAAAAG-----GAGQGGYGGLGSQG----TSGRGG--LGGQGAGAA 68
 AFSGIPGVGPFGGQQPGVPLGYPIKAPKLPGGYGLPYTNGKLPYGVAGAGGKAGYPTGTG
 GQGGYGGLGSQGTSG-----
 LGAGVGAGGKPGKVPGVGLPGVYPGGVLPGTGARFPGVGVLPGVPTGTGVKAKVPGGGGG
 AAAAAAAAGGAGQGGYGGL------GSQG-----TSGRGGLGGQGAGAAAAAA 111
 GGLGGGALGPGGKPPKPGAGLLGAFGAGPGGLGGAGPGAGLSYASRPGGVLVPGGGAGAA 112
AGAAAAAAAAAA ---GGAGQG----GYGGLGSQGTSGR----GGLGGQGAGAAAAAAAAA
 AAYKAAAKAGAGLGGIGGVPGGVGGVPGAVGVGGVPGAVGGIGGIGGLGVSTGAVVPQ
 requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
 protein; Connective
 Conservative
 splicing.
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 21
864
307
308
823
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 PubMed=2971041;
 26.5%;
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 BY SIMILARITY.

ELASTIN.

MISSING (IN CERTAIN CLONES).

MISSING (IN CERTAIN CLONES).

MISSING (IN CERTAIN CLONES).

MISSING (IN CERTAIN CLONES).
 Score 939;
Pred. No. 1.
 ----PGGYG----PGQQTSGRGGLGGQ-----
 tissue;
 Mismatches
 Repeat;
 DB 1;
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LY AND RECOVER
E CROSS-LINKED
 Signal;
 Length 864;
 Indels 198;
 EMBL outstation
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Q10637;
Q10637;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV1325C PRECURSOR.
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C., Ell, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.:
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393537-544(1998).
This SWISS-PROT entry is copyright. between the Swiss Institute of Biol
 MEDLINE=98295987; PubMed=9634230;
 STRAIN=H37RV;
 Actinomycetales;
NCBI_TaxID=1773;
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 Mycobacterium tuberculosis.
 RV1325C OR MTCY130.10C
 SEQUENCE FROM N.A.
 591
 387
 471
 413
 812 ARPGFGLSPIYPGGGAGGLGVGGKPPKPYGGALGALGYQGGGCFG
 705
 460
 SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY; PGRS
 SUBFAMILY.
 GGQGAGAAAAAAAAAAGGAGQGG-----YGG-LGSQGTSGPGGYG 667
 GAGGLGAGGLGAGGVIPGAVGLG--GVSPAAAAKAAKYGAAGLGGV--LGARPFPGGGVA
 GQGGY--GGLGSQGT-SGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGL
 LGGVPGGVAGGAPAAAAAKAAAKAAQYGLGGAGGLGAGGLG-----AGGL
 LGGQGAGAA--AAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGA 571
 AGAGVPGFGAGAVPGSLAASKAAKYGAAGGLGGPGGLGGPGGLGGPGGFG-----GPGG
 GRGGLGGQGAGA-----AAAAAAAAAGGAGQGGYGGLGSQ-GTSGPGGYGPGQQTSGRGG
 GTGLVPGDLGGAGTPAAAKSAAKAAAKAQYRAAAGLGAGVPGLGVGAGVPGFGAGAGGFG
 GVPGAGTPAAAAAAAAAAKAAKAGQYGLGPGVGGVPGGVGGLPGGVGPGGVTGIGTGP
 GLGGQGAGAAAAAAAAA
 AAAAAAAAKAAKYGAGGAGTLGGLVPGAVPGALPGAVPGALPGAVPGALPGAVPGVPGTG
 GAGAAAAAAAAGGAGQGGYGGL------
 GGLGGQGAGAAAAAAAAAAGGAGQGGYGGLG--SQGTSGPGGYGPGQQTSGRGGLGG--Q
 AKAAKYGAAGGLVPGGPGVRVPGAGIPGVGIPGVGGIPGVGGIPGVGGPGIGGP
 AGGAGQGGYGGLGSQGTSGR-GGLGGQGAGAAAAAAAAAGG-AGQGGYGGLGSQGTSGR
 -RGGLGGQGAGAAAAAAA-----AAAG-GAGQGGYG-----GLGSQGTS
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Pfam; PF00934; PE; 1

Hypothetical protein; Repeat;
SIGNAL 1
 the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 EMBL; Z73902; CAA98089.1;
HSSP; P19972; 1KVD.
 TubercuList; Rv1325c; -.
 291
 255
 182
 126
 Local Sin
 99
 22
 28
 GGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAAGGA 483
 PGGYGPGQQTSGI
 GTSGRGGLGGQGAGAAAAAAAAAAAAGGAG----QGGYGGLGSQGTSGRGGL---GGQGAGA
 GAGGAGGLLFGSGGAGGPGGVGNTGTGGLGGDG-GAAGLFGAGGIGGAGGPGFNG----
 GAAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGL
AGG
 --AGMVGNGGDGGAGGASVVANGGVGGSGGN--
 AAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAGGAGQGGYGGLGS-QGTSG
 -ETAGDGGAGGN-----AGLLNGDGGAGGAGGLGTAGDGGNGGKGGK
 GQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGLGS
 GIGGTGGTGLGAPDPGGTGGKGGVGGIG-----GAGALFGPGGAGGTGGFGASSADQMA 404
 AAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGLG-SQGTSGR
 GFGVSGSAGGNGGTGGDGGIFTGNGGTGGTGGTGTGNQLVGGEGGAGGAGGNAGILFGAG
 AAAAAAAAGGAGQGGYGGL--GSQGTSGPGGYGPGQQ-TSGRGGLGGQGAGAAAAAAA
 AAAAAAAGGA--GQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGLGSQ 254
 AAAAAAAAAGGA--GQGGYGGLGSQG-TSGPGG----YGPGQQTSGRGGLGGQGAGAAAA 196
 GSQGTSGRGGL---GGQGAGA-AAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGA 143
 GSTLGAANAAALGP-----TTELLAAGADEVSAAIASLFAAHGQA----YQAV
 GGIGGSG---GSGGAAKLIGDGGAGGTGGDSVRGAAGSGGTGGTG------GLI
 PGTGQAGGAGGLLYGNGGAGGSGAPGQAGGPGGAAGLFGNG----GAGGAGGDGPGNGAA
 SAQMSAFHAQFVQTFTAGAGAYASAEAAAAAPLEGLLNIVNTPTQLLLGRPLIGNGANGA
 ·GAGGAGGR-SGLFEVLAAGGAGGTGGLSVNGGTGGTG--GTGGGGGLFSNGGAGGAG
 Similarity
 114
603
 Conservative
 Ą.
593
 675
 603
49575
 603
 24.5%;
 GTGIEFGSVGGAGGAGGNAAGLSGAGGAGGA--GGFG----
 MW;
 35;
 Score 869; DB 1;
Pred. No. 1.3e-32;
5; Mismatches 256
 GLY-RICH
 HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV1325C.
 POTENTIAL
 Signal
 4F9BCB82B07AE964 CRC64;
 -ATLIGNGGNGGNGGVGSAPGKGG
 Length 603;
 Indels 126;
 Gaps
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 p10496;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8
 DOMAIN
DOMAIN
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 association of the protein with the vascular system EMBO J. 7:3625-3633(1988).
 Phaseolus vulgaris (Kidney bean) (French bean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae
Fabales; Fabaceae; Papilionoideae; Phaseolus.
 EMBL; X13596; CAA31932.1;
 -!- FUNCTION: RESPONSIBLE FOR PLASTICITY OF THE CELL WALL (POTENTIAL).
-!- SUBCELLULAR LOCATION: CELL WALL (POTENTIAL).
-!- DOMAIN: THE REPEARED DOMAINS OF THE PROTEIN FORM A BETA-PLATED SHEET CONFIGURATION.
-!- SIMILARITY: THE N-TERMINAL SIGNAL SEQUENCE OF ABOUT 30 AA SHOWS ABOUT 60% HOMOLOGY TO THAT OF THE GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN GRP 1.0.
 STRAIN-CV. TENDERGREEN,
MEDLINE-89091109; PubMed-3208742;
Keller B., Sauer N., Lamb C.J.;
Keller B. (Sauer N., Lamb C.J.;
"Glycine-rich cell wall proteins in
 GRP2_PHAVU
 SEQUENCE
 CHAIN
 SIGNAL
 cell wall;
 PIR; SO
 SEQUENCE FROM N.A.
 HSSP; P30129; 4DPV.
 327
 191
 267
 152
 207
 107
 148
 63
 19
 LGSQGTSGPGGYGPGQQTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG
 QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQG
 GVAYGGGGERGGYG--GGQGGGAGGGYGAGGEHGIGYGGGGGGSGAG------G
 GAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGL
 GGGYNAGGAQG-----GGYGTG------GGAGGGGGGG----GDHGGGYGGGQG
 G--GYAGEHGVVGYGGGS-----
 GSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAA
 GVCSARRALLTLDAGYGLGHGTG------GGYGG-----AAGSYGGGGGGGGGGGG
 AG--
 AGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGG
 Similarity
 1820; S01820.
 Structural protein;
 Conservative
 33
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 STANDARD;
 GGAG-GGYGGGGEHGGGGGGGGGGGG-GAGGGYGAGGEHGGGAGGGQGGG
 465
359
 30
465
 36683 MW;
 24.1%; Score 853.5; DB 1; 39.9%; Pred. No. 5.2e-32; live 16; Mismatches 170;
 POTENTIAL.

GLYCINE-RICH CELL WALL STR
PROTEIN 1.8.

GLY-RICH.

8 X 22 AA TANDEM REPEATS.

W; B5C4A9B983B43607 CRC64;
 PRT;
 Repeat; Signal.
 bean: gene structure and
 465
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 PRECURSOR
 Rosidae;
 Indels
 Length
 STRUCTURAL
 Spermatophyta;
 (GRP 1.8).
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RESULT 13
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 gene for human elastin.";
Blochem. Cell Biol. 69:185-192(1991).
II FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
II SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER INTO AN EXTENSIBLE 3D NETWORK.
IS SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
I- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE PRODUCED BY ALTERNATIVE SPLICING.
INTO THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
 MEDLINE-89274159; PubMed-2543440;
Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.
Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks
 "Primary structures of bovine elastin sequences of cDNA clones.";
J. Biol. Chem. 262:5755-5762(1987).
 SEQUENCE FROM N.A.
MEDLINE-87194772; PubMed-3032943;
Raju K., Anwar R.A.;
 Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Cei
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
 ELS_BOVIN STANDARD; PRT; 7904985; P04986; P04987; Q29421; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence up 10-MAY-2000 (Rel. 39, Last annotation ELASTIN PRECURSOR (TROPOELASTIN).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
 alternative splicing of elastin mRNA Biochemistry 28:2365-2370(1989).
 TISSUE-Nuchal ligament; MEDLINE-89274159; PubMe
 Manohar A., Shi W., Anwar R.A.; "Partial characterization of bovine elastin gene;
 MEDLINE-91234332;
 SEQUENCE OF 1-27 FROM N.A.
 Rosenbloom J.;
"Structure of the bovine elastin gene
 SEQUENCE OF 1-27 FROM N.A.
 Bos taurus (Bovine).
 436
 307
 447
 399
 567
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 507
 239
 387
 AG-----
 GGGGYG-----AGGAHGGGYGGGGGIG----GGHG 461
 GLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYG 667
 GLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAG
 AAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG
 EHGGGYG-
 QTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAA
 QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQ
 AGGGQG
 --GDHGAAGYGG-----GEGGGGGGGGGGG-----YGDGGAHGGGYGG-----
 -GGQGGG----AGGGYGTGGEHGGGYGG-----GQGGGGGYGAG
 -GGYGAGGEHGGGAG--GGYGAGG----GGYGAGGEHGGG
 PubMed=2031719;
 Cetartiodactyla;
 Chordata; Craniata; Vertebrata; Euteleostomi;
 -GGAG----GGYGAGGEHGGGAGGGQG
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 Ruminantia; Pecora; Bovoidea;
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EMBL; K03506; AAA30506.1; --
EMBL; J02855; AAA30776.1; --
EMBL; M58652; AAA30719.1; --
FIR; A26728; A26728.
FIR; B26728; B26728.
FIR; C26728; C26728.
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 the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
 MOD_RES
 SIGNAL
 HSSP; P04002; 1WFA. Structural protein;
 CHAIN
 140
 56
 32
 3 SMTGGQQMGRGSMASGRGGLGGQGAGAAAAAAAAAAAAGG-AGQGGYGGLGSQGTS-----
 TSGR----GGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRG--GLGGQGAGAAA
 GAGQGGYGG-----LG--SQGTSGPGGYGPGQQTS-----GRGGLGGQGAGAAAAAAA
 G-GAG--QGGYGGLGSQGTSGRGGLGGQGA------GA-----AAAAAAAAAG
 GVGAGVKPGKVPGVGLPGVYPGGVLPGAGARFPGIGVLPGVPTGAGVKPKAQVGAGAFAG
 GGFFGAGGGAAGAAAYKAAAKAGAAGLGVGGI------GGVGGLGVSTGAVVPQLGA
 IPGVGPFGGQQPGLPLGYPIKAPKLPAGYGLPYKTGKLPYGFGPGGV-------
 AVPGGVPGGVFFPGAGLGGLGVGGLGPGVKPAKPGVGGLVGP----GLGAEGSALPGAFP
 -GRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAA
 tive
 Similarity
 12
747
 splicing
 Conservative
 26
747
747
105
109
252
271
271
275
324
400
400
 Connective tissue;
 21.9%; 38.4%;

 MW.
 33;
 OXIDATIVE DEAMINATION.
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OXIDATIVE
OXIDATIVE
OXIDATIVE
OXIDATIVE
 Score 777.5;
Pred. No. 1.
 Mismatches
 (See http://www.isb-sib.ch/announce/
 Repeat;
 nes 275;
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 MEDLINE-84270667; PubMed-6087149; Baer R., Bankler A.T., Biggin M.D., De Gibson T.J., Hatfull G., Hudson G.S., Tuffnell P.S., Barrell B.G.; "DNA sequence and expression of the B9 Nature 310:207-211(1984).
 Epstein-barr virus (strain B95-8) (Human herpesvirus Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus
 BKRF1
 Sample J., Hummel M., Braun D., Birkenbach M., Kieff E.;
"Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear
proteins: a probable transcriptional initiation site.";
 21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-DEC-1998 (Rel.
 EΒV
Bochkarev A., Barwell J.A., Pfuetzner Edwards A.M., Frappier L.; "Crystal structure of the DNA-binding
 MEDLINE-90266473; PubMed-2161150;
Pett1 L., Sample C., Kieff E.;
"Subnuclear localization and phosphorylation
latent infection nuclear proteins.";
 SEQUENCE OF 1-26 FROM N.A. MEDLINE-86259739; PubMed-3
 SEQUENCE FROM N.A.
 EBNA-1 NUCLEAR PROTEIN
 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) MEDLINE=96006523; PubMed=7553871;
 SUBCELLULAR LOCATION.
 NCBI_TaxID-10377
 467
 418
 367
 310
 297
 645
 AAAGGAGQGGYGGLGSQGTSGRGGLGGQ----GAGAAAAAAAAAAGGAGQGGYGGLGSQG
 PIG-GGAGGLG-------VGGKPPKPFGGALGALGF--PGG
 TSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGG-LGSQGTSGPGG 665
 IGLGPGGVIGAGVPAAAKSAAKAAAKAQFRAAAGLPAGVPGLG-VGAGVPGLGVGAGVPG
 AIPGLPGVGGVPGVGIPAAAAAKAAAKAAQFGLGPGVGVAPGVGVVPGVGVVPGVGVAPG
 --QGTSGRGGLGGQGAGAAAAAAAAAAAAG---GAGQG------GYGGLGSQGTS--
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 LGVGAGVPGPGAVPGTLAAAKAAKFGPGGVGALGGVGDLGGAGIPG-GVAGVVPAAAAAA
 SGRG-GLGGQGA--GAAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAA
 -GGAGOGGYGGLGSQGTSGRGGLGGOG-AGAAAAAAAAAAAGGAGOGGYGGLGS-----
 -----GVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVPGALSPAATAKAAKAAK
 Natl. Acad.
 -GRGGLGGQGAGAAAAAAAAA------GGAG-QGGYGGLGSQGTSGPG-GYGPGQQT
 176:563-574(1990).
 STANDARD;
 . 01, Created)
. 01, Last sequence 37, Last annotations.
 PubMed-3460083;
 Sci. U.S.A. 83:5096-5100(1986).
 Last sequence update)
Last annotation update)
 PRT;
 Deininger P.L., Fi
., Satchwell S.C.,
 B95-8 Epstein-Barr
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 EMBL; V01555; CAA24816.1; -
EMBL; M13941; AAA45889.1; -
PIR; A03773; QOBE31.
PIR; S33021; S33021.
PDB; 1VHI; 23-DEC-96.
TRANSFAC; T00211; -
 virus origin-binding protein EBNA 1.";
Cell 83:39-46(1995).
Cell 83:39-46(1995).
IN LATENT CYCLE. EBNA-1 FUNCTIONS IN
MAINTENANCE REPLICATION OF EBV EPISOME. TRANSACTIVATING
FOR THE ORIGIN AND ENHANCER FUNCTIONS OF ORIP.
-1- SUBCELLULAR LOCATION: NUCLEAR. FREE IN THE NUCLEOPLASM,
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 Nuclear protein; DNA-binding; Transcription regulation;
 116
 D-structure.
 120
 175
 447
 403
 188
 159
 283
 223
 63
 5
 WITH THE NUCLEAR MATRIX.
 ASSOCIATED WITH THE CHROMATIN AND HARDLY, IF AT
 GAGQGGYGGLGSQG-TSGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGY
 GPRHRDGVRRPQKRPSCIGCKGTHGGTGAG--AGAGGAGAGGAGAGGAGGAGAGG-GAGGAG
 GLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQQTSGRGGLGGQGAGAA
 GAGGAGAGG
 GAGGAGAG-------GGAGAGG-----
 GLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAAGGAG
 GPGTGPGNGLGEKGDTSGPEGSGGSGPQRRGGDNHGRGRGRGRGRGG--GRPGAPGGSGS
 AAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQGGYGGLGSQGTSGRG
 QGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPGQ
 GPGQQTSGR-----
 STGPRGQGDGGRRKKGGWFGKHRGQGGSNPKFENIAEGLRALLARSHVERTTDEGTWVAG
 YGGLGSQGTSGRGGLGG----
 QSSSSGSPPRRPPPGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGP
 QGTS
 -----SGGRGRGGSGGRGRGSGGRRGRGRGRARGGSRERARGRGRGRGEKRPRSPSS
 --GGAGGAGGAGAG
 Similarity
 641 AA;
 Conservative
 87
 -GAGGAGGAGAG------GGAGAGG
 -GR----
 352
56427 MW;
 21.5%;
 - AGAGGAGGAGGAGGAGGAGGAGGG----GAGGAGAGG
 -GGLGGQGAGAAAAAAAAAGGAGQGGYGGLGSQGTSGRG
 -OGAGAAAAAAAAAAAGG--
 22;
 Score 763; DB 1
Pred. No. 5.8e-2
22; Mismatches 2
 GLY/ALA-RICH.; 4D161653E16FC341 CRC64;
 -GGLGGQGAGAAAAAAAAAAAGGAGQGG
 -GAGGAGGAGAG-GGAGGAGGAG
 209;
 -----GAGGAGAG-
 Length
 Indels 186;
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QGGYGGLGS-----QGTS------GPGGY--GPGQQTSGIR

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ELS_CHICK
P07916;
01-AUG-1988 (
01-OCT-1986 (
ELASTIN PRECU
 EMBL; M18633; AAA48761.1; -
EMBL; M21880; AAA49082.1; -
EMBL; M21880; AAA49108.1; -
PIR; A27264; A27264
PIR; A26601; A26601.
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 SEQUENCE FROM N.A.

MEDLINE-87242320; PubMed-3593675;

Bressan G.M., Argos P., Stanley K.K.;

"Repeating structure of chick tropoelastin
DNA cloning.";
 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
 MEDLINE-87297534; PubMed-3502711;
Tokinitsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T.;
"Sequence analysis of elastin cDNA from chick aorta and
tissue-specific transcription of the elastin gene in developing
embryo.";
 Structural
 embryo.
 SEQUENCE OF 457-750 FROM
 Blochem. Blophys. Res. Commun.
 SEQUENCE OF 85-750 FROM N.A. MEDLINE-88309083; PubMed-2841924;
 Alternative
 HSSP;
 Baule V.J., Foster J.A.;
"Multiple_chick_tropoelastin mRNAs.";
 Biochemistry 26:1497-1503(1987).
 507
 h. Blochem. Blophys. 256:455-461(1987).
FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS A NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED INTO AN EXTENSIBLE 3D NETWORK.
SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO FORMS OF CELASTIN THAT ARE PRODUCED BY ALTERNATIVE SPLICING.
PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
 VFVYGGSKTSLYNLRRGTALAIPQCRLTPLSRLPFGMAPGPGPQPGPLR
 P04002; 1WFA.
 1988 (Rel. 08, Created)
1988 (Rel. 08, Last sequence update)
1996 (Rel. 34, Last annotation update)
1996 (TROPOELASTIN) (FRAGMENT).
 protein;
 s splicing.
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 G-GQGA------GAAAAAA---AAAAGGAGQGGYGGLGSQGTSGRGGL---GGQGAGAAA
 -------QGTSGRGGLGGQG--AGAAAAAAAAAGGAGQGGYG--GLGSQGTSGRGG
 GGAGQGGY-----GGLGSQGTSGPGGYGPGQQTSGRGGLGGQQGAGAAAAAAAAAAAAG-GA-
 AAAAAAAG------GAGQGGYGGLGSQGT--SGRGGLGG--QGAGAAAAAAAAAAA
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 AIPGGGVPGGGFFPGAGVGGLGAGLGAGLGAGLGAGLGRFLKPGVSGLGGLGPLGLQPGAGVGGL
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 --GQGGYGGLG----SQGTSGRGGLGGQGAGAAAAAAAAAAAGGAGQG----
 Similarity
 Conservative
 AA;
 501
536
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OXIDATIVE DEAMINATION (POTENTIAL)
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 Score 709; DB 1; I
Pred. No. 1.5e-25;
9; Mismatches 276;
 Length 750;
 Indels 196;
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Search completed: July 3, 2001, 15:10:47 Job time: 747 sec

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Result
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 Post-processing: Minimum Match 0%
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Listing first 45 su
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 Scoring table:
 OM protein -
 Total number of hits satisfying chosen parameters:
 Title:
 Perfect score:
 9
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 US-09-490-291-6
3543
 SPTREMBL_16:*
 425026 seqs, 132305027 residues
 GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
 MASMTGGQQMGRGSMASGRG.....TSGIRIRAPSTSFEHHHHHH
 sp_organelle:*
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sp_bacteria:*
 sp_unclassified:*
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 Length
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591	606	639	618	584	576	922	902	610	484	904	694	626	.667	923	1729	810	1011	741	714	731	636	783	837	767	882
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## ALIGNMENTS

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 O46172 PRELIMINARY; PRT; 617 AA.
O46172;
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O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DRAGLINE SILK PROTEIN SPIDROIN 1 (FRAGMENT).
Nephila clavipes (Orb spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
NCBI_TaxID-6915;
 Insect Biochem. Mol. Biol. 0
EMBL; U37520; AAC04504.1; -.
NON_TER 1 1
NON_TER 617 617
 "Sequence conservation in the C-terminal region of spider silk proteins (Spidroin) from Nephila clavipes (Tetragnathidae) and bicentenarius (Araneidae).";
J. Biol. Chem. 269:6661-6663(1994).
 SEQUENCE
 Beckwitt R., Arcidiacono S., Stote R.; Insect Biochem. Mol. Biol. 0:0-0(1998).
 SEQUENCE FROM N.A. MEDLINE-94165058; PubMed-8120021;
 SEQUENCE FROM N.A.
 Beckwitt R., Arcidiacono S.;
58
 62 GQGAGAAAAAAAAGGAGQGGYGGLGSQGTSGRGGLGGQGAGAAAAAAAAAAGGAGQGG
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 N
 ANAGGAGQGGYGGLGSQGAGRGGQGAG----AAAAAAAGGAGQGGYGGLGSQG-AGRGGLG
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 O46171 PRELIMINARY; PRT; 544 AA.
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O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 16, Last sequence update)
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Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
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MEDLINE-98148687; PubMed-9487707;

Arcidiacono S., Mello C., Kaplan D., C

"Purification and characterization of expressed in Escherichia coli.";

Appl. Microbiol. Biotechnol. 49:31-38(
 MEDLINE-90384959; PubMed-2402494;
Xu M., Lewis R.V.;
"Structure of a protein superfibe:
Proc. Natl. Acad. Sci. U.S.A. 87:
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Beckwitt R., Arcidiacono S., Stote R.;
Insect Biochem. Mol. Biol. 0:0-0(1998)
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 143
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 superfiber: spider dragline J.S.A. 87:7120-7124(1990).
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 O17434 PRELIMINARY; PRT; 988 AA.
O17434; O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
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Matches 359
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076786;
01-NOV-1998
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01-OCT-2000
 MEDLINE-98200471; PubMed-9541398;
COlgin M.A., Lewis R.V.;
"Spider minor ampullate silk proteins contain new repetitive sequences and highly conserved non-silk-like 'spacer regions'.";
Protein Sci. 7:667-672(1998).
EMBL; AF027735; AAC14589.1; -.
InterPro; IPR00341; PRION.
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 Sezutsu H., Tamura T., Yukuhiro K.;
"Characterization of the full length fibroin gene of a wantheraea pernyi.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF083334; AAC32606.1;
SEQUENCE 2639 AA; 216056 MW; 2EE3310DEEB09B9A CRC64;
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Ra Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Ra Badcock K., Basham D., Brown D., Chilingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Cliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E. Taylor K., Whitehead S., Barrell B.G.; Taylor K., Whitehead S., Barrell B.G.; Tochphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Lature 393:537-544(1998).

Rebb: ALO22022; CAA17751.1; -.
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 01-JUN-1998
01-JUN-1998
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053559;
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Interpro; IPR002202; -.
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 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).

EMBL; AL021942; CAA17449.1; -.
 01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
PGRS-FAMILY PROTEIN.
 Prodom; PD001223; -, 1.

PROSITE; PS00188; PFKB_KINASES_1: UNKNOWN_2.

PROSITE; PS00118; SUBTILASE_SER; UNKNOWN_1.

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InterPro; IPR002173; -.
Pfam; PF00934; PE; 1.
 MEDLINE=98295987; PubMed=9634230;
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O1-JUN-1998 (TrEMBLrel. 06, C
O1-JUN-1998 (TrEMBLrel. 06, L
O1-OCT-2000 (TrEMBLrel. 15, L
PGRS-FAMILY PROTEIN.
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Baddock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rafandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
 InterPro; IPR000084; -.
InterPro; IPR002173; -.
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Mycobacterium tuberculosis.
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 Actinomycetales;
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STRAIN=H37RV;
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 Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLeen J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.
Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
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Nature 393:537-544(1998).
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 Q9NHW2;
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Q1-OCT-2000 (TrEMBLrel. 16, Last annotation update)
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 Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
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 Science 287:1477-1479(2000).
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Hayashi C.Y., Lewis R.V.;
"Molecular architecture and evolution of a modular spider silk
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MEDLINE-98295987; Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Elglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
 053395;
 01-JUN-1998 (TrEMBLrel. 06, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PGRS-FAMILY PROTEIN.
PE_PGRS OR MY3345C OR MTV004.01C-MTV016.45C.
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Interpro; IPR000084; ...
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Pfam; PF00934; PE; 1.
ProDom; PD001223; ..; 1.
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 Submitted (JUN-1998) to the EMBL/GenBank/DDBJ EMBL; AL021841; CAA17117.1; -. HSSP; P00441; ISSS.
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788F0B2095587592
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Length 1538;

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 "Structures of mollusc shell framework proteins.";
Nature 387:563-564(1997).
EMBL; D86074; BAA20466.1; -.
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Sudo S., Fujikawa T., Nagakura T., Ohkubo T.,
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 Q9NHW4 PRELIMINARY; PRT; 2249 AA. Q9NHW4; O1-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence up 01-MAR-2001 (TrEMBLrel. 16, Last annotation FLAGELLIFORM SILK PROTEIN (FRAGMENT).
 InterPro;
PROSITE;
 SEQUENCE FROM N.A.
MEDLINE-20156766; PubMed-10688794;
Hayashi C.Y., Lewis R.V.;
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 Science 287:1477-1479(2000).
EMBL; AF218621; AAF36090.1; -.
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	TSGRGGLGGQGAGAAAAAAAAAAGGAGQGGYGGLGSQGTSGPGGYGPG 669	622	Qy
1384	AGAGLGGVGAGGSSGLSTASAASGASGAGEVIVINDRSSAASAAAGSGASGLGGLGLGG	1325	ф
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DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DT 10-MAR-2001 (TREMBLrel. 16, Last annotation update)
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RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV; PubMed-9634230;

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 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hanlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
EMBL; 25844; CAB09271.1;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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/SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
 /SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1990.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1992.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1995.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1996.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1997.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA2000.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA2001.DAT:*
 MASMTGGQQMGRIRIRGYGG......
 Length
 506
506
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 119
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 ij
 AAR14308
AAY40097
AAR99055
AAY40102
AAY40101
AAR99057
AAR99053
 AAW27178
AAW53346
AAY59070
 AAY401,00
 SUMMARIES
 model
 .GLSGCDVLIQALLGHHHHHH 528
N. clavipes draglin
Spider silk protei
Spider dragline va
Polymer of an anal
Polymer of an anal
Spider dragline va
Spider dragline va
Polymer of an anal
 Description
 Nephila clavipes s
Nephila clavipes s
N. clavipes spider
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ECB-CIDITI	V 3 C 3 C 0		1000	ر	ייי	2
						'n :
FCB-SLPIII		21	979	34.1	•	44
FCB-SLPIII	AAY78285	21	766	34.1	•	3
FCB-SLPIII		18	766	34.1	•	42
Amino acid		19	695	34.1	921.5	41
FCB-SLP protein fr		22	1038	34.2	•	0
Repetitive		22	1038	•	•	39
Fibronectin cell		17	1038		922.5	
SLP-C protein sequ		22	1332	34.4	929	7
Repetitive protein	AAB72729	22	1332	34.4	929	
Silk like	AAR95109	17	1332	34.4	929	5
Adhesion protein.		16	980	35.1	946.5	4
SEPL4 protein comp	Þ	9	1059	35.4	955.5	ω
SELP4 amino acid		21	1101	35.6	962.5	32
SLP4 synthetic pro		18	1059	35.6	962.5	-
		14	1059	•	962.5	0
Amino acid sequenc	AAW53524	19	1023		962.5	9
Polymer of an anal	AAY40103	20	714	•	970	8
Spider dragline va		16	714	٠	970	27
Amino acid sequenc		19	1178		972	26
Silk-like		14	1178	•	972	25
SLPIII protein seq		22	1177	36.0	972	24
Repetitive		22	1177	•	972	
SlpIII amino acid	AAY78277	21	1177	36.0	972	22
Silk-like		18	1177	•	972	
11k	AAR95105	17	1177	٠	972	20
SLP III (Silk-fibr	AAR05307	11	1177		972	19
SlPIII protein com	AAP80940	9	1177	36.0	972	18
Peptide dendrimer	AAB70188	22	465	•	w	17
N. clavipes spider	AAY59071	21	595		1144	16
Nephila clavipes		19	595	•	1144	15
N.clavipes draglin	AAR14309	12	595	42.4	1144	14
Spider silk	AAY40099	20	615	45.7	1234	13
	AAR8016	16	831	49.8	1344	12

## ALIGNMENTS

RESULT AAW27178

-

AAW27178 standard;

Protein; 646

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```
WPI; 1997-179272/16.
N-PSDB; AAT85356.
 High strength film; fibre; woven article; parachutes; sails;
absorber; body armour; heavy metal; biological weapon; chemical;
New opt. multimerised DNA sequences encoding spider silk protein contg. both repetitive and non-repetitive sequences, useful for
 Nephila clavipes spider silk protein
 09-DEC-1997 (first entry)
 AAW27178;
 Basel RM, Elion GR;
 22-AUG-1995;
 22-AUG-1996;
 06-MAR-1997.
 WO9708315-A1.
 Nephila clavipes.
 (BASE/) BASEL R M.
(ELIO/) ELION G R.
 flavour; fragrance; Nephila clavipes
 95US-0517694.
 96WO-US13767.
```

making

high strength films, fibres, woven articles

etc

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CC a process has been developed for the production of a DNA fragment CC encoding silk protein. The process involves: (a) selecting target DNA, CC from a silk-producing spider, that contains many repetitive and non-cc range of the target (b) selecting a single-stranded DNA primer of at CC least 10 nucleotides with a sequence that is complementary to a region CC of the target; (c) repetitively combining the primer with melted target CDNA, incubating the mixture with nucleotides and a DNA polymerase with CC proofreading activity to produce a DNA fragment which is complementary CC to the target and is at least 2 kb long. The present sequence encodes CC to the target and is at least 2 kb long. The present sequence encodes CC used to make fibres, films, woven articles, e.g. for use in parachutes, CC weight (90-250 kD) of spider silk proteins can be produced on a CC commercial scale (at over 2 g/l cell mass). It has better tensile CC strength and elasticity than silkworm silk. Inclusion of both repetitive CC end non-repetitive regions enginees isolation of stabile connections.
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 AAW53346
 RESULT
 Matches
 Query Match
Best Local Similarity
 Sequence
AAW53346
 497
 359
 299
 239
 169
 179
 119
 583
 463
 377
 407
 283
 229
 109
 61
 60
 σ
 non-repetitive regions ensures isolation of stable clones
 N
 GGQQMGRIRI-----RGYGGLGGQGAGAGQGAGAAAAAAAGGAGQGGYGGLGSQGAGRGGQG
 SNVVSQIGASNPGLSGCDVLIQALL 521
 GAG--AAAAAGGAGQGGLG----GQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAA
 GGQGAGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGSGGQGAGAAAAAAAGGAGQGGYGGL
 AAAAVGAGQGGYGGVGSGASAASAASRLSSPQASSRVSSAVSNLVASGPTNSAALSSTI 496
 AAAGGYRQGGYGGLGSQGAGRGGQGAGAAAAAAGGAGQGGTGGLGGQGYGAGGLGGQGAG
 aaaag-----gagqggygglgsqgagrgglggqgag--aaaaaaggagqggyggl
 AGAAAAAAG-----GAGQGGYGGLGSQGAGRGGLGGQGAG--AAAAAGGVGQGGL
 ggqgagaaaaaaaggagqgglggqgagqag-aaaaaaggagqggygglgsqgagrggqg
 snvvsqigasnpglsgcdvliqall
 aaaaggagggggggggsgasaasaasrlsspgassrvssavsnlvasgptnsaalssti
 ggqgagqggygglgsqgsgrgglggqgagaaaaaaggagqgglggqgagqgag----aaa
 AAAAGGAGQGGYGGQGAGQGGYGGLGSQGAGGGGGGGGGAGAAAAAAAAGGAGQ-----
 ggqgagqgagaaaaaggagqggygglgsqgagrggsggqgagaaaaaggagqggyggl
 484;
 2;
standard;
 646 AA;
 Conservative
 1; 57pp; English
 Protein;
 85.98;
85.78;
 718
 Score 2319; DB 18;
Pred. No. 2e-152;
1; Mismatches 14;
 ξ
 Indels
 Length
 646;
 66;
 Gaps
 . 376
 168
 178
 108
 118
 60
 436
 462
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 358
 282
 298
 228
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 Query Match
Best Local
 Matches
 15-APR-1991;
20-APR-1990;
04-OCT-1994;
19-APR-1995;
 The present sequence represents a spider silk protein from the present invention. Spider silk proteins, and peptide fragments within the proteins, can be produced and purified independently and can then be mixed and made into fibres that have higher tensile strengths and elasticity than naturally occurring fibres. The fibres can be used in mixed composites. The invention allows the two naturally occurring Nephila clavipes silk proteins to be produced independently so that they can later be combined to form silk fibres of high tensile strength
 06-JUL-1998
 Hinman MB,
 17-MAR-1998
 US5728810-A
 Nephila clavipes
 Spider;
 Nephila
 AAW53346;
 Sequence
 Claim 1; Column 29-34; 68pp; English.
 Recombinant spider silk proteins - useful for
 WPI;
 (UYWY-) UNIV
 19-APR-1995;
 and elasticity.
 167
 139
186
 199
 66
 79
 22
 6 GGQQMGRIRIRGYGGLGGQGAGQGAGAAAAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAAA
 GLGSQGAGRGGLGGQGAGA------
 AAAGGAGQGGYGGLGSQGAGRGGLGGQGAG--AAAAAGGYGQGGLGG---QGAGQGA-GA
 ggqgagq----ggygglggqgaggagaaaaaaggagqggygglgsqgagrggqgagaaa
 1998-270437/24
 AAAAAGGAGQGGYGGLGSQGAGRGGSGGQGAGAAAAAAG------
 glgsqgagrgglggqgagaaaaaaaggagqgglggqgagqgagasaaaaggagqggyggl
 aaaggaggggggglgsqgagrgglggggagaaaaaaaggaggggggglgnggagrgggga
 479;
 Nephila clavipes; silk protein; tensile strength; elasticity.
 clavipes spider silk protein.
 AAV23249
 Similarity
 718
 Lewis RV,
 Conservative
 WYOMING
 (first entry)
 90US-0511792.
94US-0317844.
95US-0425069.
 A,
 91US-0684819
 95US-0425069
 ---AAAAAAGGAGQGGYGGLGGQGAGQGGYGGLGSQGAGRGGLGGQGAGA
 81.3%;
 ž
 X
 4;
 Score 2196; DB 19;
Pred. No. 6.4e-144;
4; Mismatches 10;
 tandem repeat; fibre; dragline;
 making
 Indels 188;
 Length
 fibres
 -GAGQGGYG 166

 Gaps
 119
 198
 138
 78
 65
 317
 232
 185
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81.3%; 70.3%;

Score 2196; Pred. No. 6.

DB

Length

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RESULT
AAY59070
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 The invention provides isolated cDNA molecules coding for spider silk proteins. The spider silk proteins are characterized by repeating alpha and beta regions and optional variable regions. The DNA sequences are useful in the production of spider silk protein by recombinant DNA techniques. The recombinant spider silk proteins may be used for the production of fibers. The present sequence represents the spider silk protein 1, derived from the major ampullate gland of Nephila clavipes.
 Claim 1; Fig 6A-D; 65pp; English.
 the
 Hinman MB,
 04-OCT-1994;
 US5989894-A.
 Spider silk protein;
 N. clavipes spider silk protein
 08-MAR-2000
 AAY59070;
 AAY59070 standard;
Sequence
 Isolated DNA, vector and transformed cell encoding the production of spider silk protein
 (UYWY-) UNIV WYOMING
 15-APR-1991;
20-APR-1990;
 23-NOV-1999
 Nephila clavipes
 318
 674
 486
 614
 426
 558
 366
 498
 337
 438
 325
 378
 285
 ω
 2000-061225/05
)B; AAZ38195.
 PTNSAALSSTISNVVSQIGAS 506
 AAGGAGGGGYGG---QGAGQG--------GYGGLGSQGAGRGGLGGQGAGA
 aaaaggagqgglggqgagqagaaaaaggagqggygglgsqgagrgglggggagavaaa
 ptnsaalsstisnvvsqigas 694
 qgag----aaaaaaggvrqggygglgsqgagrggqgagaaaaaaggagqggygglggqgv
 QGAGAAAAAAAAAAGGVRQGGYGGLGSQGAGGGGGAGAAAAAAAGGAGQGGTGGLGGQGV
 aaavgagqegirgqgagqggygglgsqgsgrgglggqgagaaaaaaggagqgglggqgag
 ------GGLGGQGAGAAAAAAGGAGQGGLGGQGAG
 <u>aaaaaaggagqggygglgnqgagrggqgaaaaaggagggggggggagragrggqgagaaa</u>
 AA-----
 aaggagqggygglgsqgagrggqgagaaaaaaggagqrgygglgnqgagrgglggggaga
 718 AA;
 Xu M,
 (first entry)
 91US-0684819
90US-0511792
 94US-0317844.
 Lewis
 Protein;
 dragline silk protein;
 R۷
 718
 ₹
 -AAAAAGGAGQ-----
 major ampullate gland; fiber.
 for and
 485
 425
 437
 324
 613
 557
 365
 497
 336
 377
 673
```

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RESULT
AAR14308
ID AAR1
XX AAR1
XX AAR1
XX AR1
XX AR1
XX IS-J
XX N-C1
XX Prot
XX Prot
XX Neph
PN EP45
XX Rep
XX 18-4
XX AR1
AR14308
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 Query Match
Best Local Similarity
Matches 479; Conserv
 N.clavipes dragline
 AAR14308 standard;
 18-APR-1991;
 protein superfibre;
 15-JAN-1992
 AAR14308
 23-OCT-1991
 EP452925-A
 Nephilia clavipes
 486
 558
 498
 438
 233
 139
 614
 426
 366
 337
 325
 378
 186
 199
 120
 674 ptnsaalsstisnvvsqigas
 259
 167
 79
 9
 22
 σ
 4
 aaavgagqegirgqgagqggygglgsqgsgrgglggggagaaaaaaggagqgglggggag
 AAAAGGAGQGGLG----GQGAGAAAAAAAGGAGQGGYGGLGSQGAGR---GGQGAGA-AAA
 AAAGGAGQGGYGGLGSQGAGRGGLGGQGAG--AAAAAGGYGQGGLGG---QGAGQGA-GA 119
 PTNSAALSSTISNVVSQIGAS
 grgglgggagaaaaggagggggggggsgasaasaasrlsspqassrvssavsnlvasg
 GAGGLGGQGAGAAAAVGAGQGGYGGVGSGASAASAASRLSSPQASSRVSSAVSNLVASG
 aaaaaaggagggggglgnqgagrggggaaaaaggagggggggglgsqgagrggggagaaa
 AA-----
 aaggagqggygglgsqgagrggggagaaaaaaggagqrgygglgnqgagrgglggqgaga
 gsqgagrggegagaaaaaaggagqggygglggqgagqggygglgsqgagrgglggqgag-
 ------AAAAAAGGAGQGGYGGLGGQGAGQGGYGGLGSQGAGRGGLGGQGAGA 232
 glgsqgagrgglggqgagaaaaaaaggagqgglggqgagqgagasaaaaggagqggyggl
 GLGSQGAGRGGLGGQGAGA------
 AAAAAGGAGQGGYGGLGSQGAGRGGSGGQGAGAAAAAAG---
 aaaggagggggglgsqgagrgglggggagaaaaaaaggaggggggglgnqgagrgggga
 Conservative
 (first
 91EP-0106217
 Protein;
 silk protein-1.
 major ampullate
 entry)
 506
 694
 718
 4.
 Mismatches
 ₽
 ----GGLGGQGAGAAAAAAGGAGQGGLGGQGAG
 silk; orb web spider
).4e-144;
nes 10;
 Indels
 ----GAGQGGYG
 188;
 Gaps
 673
 485
 425
 497
 437
 324
 377
 317
 258
 185
 198
 166
 138
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 Query Match
Best Local 9
 Matches 477;
 The spider silk protein contains a basic 34 amino acid repeat. The repeat itself contains 3 regions. The first comprises 0-9 amino acids with a sequence AGR(GGX)2. This region is not highly conserved. The second region has a sequence GAG(A)x which is highly conserved and is 8-10 amino acids long. The third segment is (GGX) and is 15 amino acids long and is very highly conserved. In most cases X is A,O, Y or L. Removal of the poly-(Ala) segments results in a silk having lower elasticity.
 DNA encoding spider silk protein-1 and 2 and variants - isolated from Nephila clavipes, for prodn. of spider silk protein and fibres having desired characteristics
 Sequence
 Claim 15;
 Lew19
 (UYWY-) UNIV OF WYOMING
 20-APR-1990;
 426
 498
 438
 378
 318
 167
 285
 120
 Local Similarity
 79
 66
 22
 6
 1991-312199/43
 AAAAGGAGQGGLG----GQGAGAAAAAAGGAGQGGYGGLGSQGAGR---GGQGAGA-AAA
 glgsqgagrgglggqgagaaaaaaaggagqgglggqgagqgagasaaaaggagqggyggl
 QGAGAAAAAAAAAAAAGGVRQGGYGGLGSQGAGGGGGGGAGAAAAAAGGAGQGGTGGLGGQGV
 ggqgagq---ggygglggqgagqgagaaaaaaggagqggygglgsqgagrggqgagaaa
 GGQQMGRIRIRGYGGLGGQGAGQGAGAAAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAAA
 aaavgagqegirgqgagqggygglgsqgsgrgglggqgagaaaaaaggagqgglggqgag
 AA-----
 aaggagqgygglgsqgagrggqgagaaaaaaggagqrgygglgnqgagrgglggqgaga
 AAGGAGOGGYGG----QGAGOG-------GYGGLGSQGAGRGGLGGQGAGA
 aaaaggaggglgggaggagaaaaaaggagggygglgsggagrgglggggagavaaa
 gsqgagrggegagaaaaaaggagqggygglggqgagqggygglgsqgagrgglggqgag.
 GLGSQGAGRGGLGGQGAGA-----
 GAGGLGGQGAGAAAAVGAGQGGYGGYGSGASAASAASRLSSPQASSRVSSAVSNLVASG
 qgag----aaaaaaggvrqggygglgsqgagrgggggagaaaaaggaggggggggggggg
 aaaaaaggagqggygglgnqgagrggggaaaaaggagqggygglgsqgagrgggggagaaa
 Page 23; 48pp;
 Xu M,
 718 AA;
 Conservative
 90US-0511792.
 Hinman
 80.8%;
 English
 4; Mismatches
 Score 2182; DB 12;
Pred. No. 5.9e-143;
4; Mismatches 12;
 ----AAAAAGGAGQ-----
 -----GGLGGQGAGAAAAAAGGAGQGGLGGQGAG
 Indels
 Length 718;
 GAGOGGYG
 Gaps
 497
 437
 284
 317
 198
 166
 78
 613
 557
 365
 377
 185
 485
 15;
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 Query Match
Best Local
 Matches
 The present sequence represents the natural spider silk protein spidroine major 1. The protein improves the moisturizing/softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins, agents that are generally difficult to administer, e.g. vitamins,
 WPI;
 Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscre
 Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens -
 Philippe M,
 11-FEB-1998;
 13-AUG-1999
 FR2774588-A1
 Nephila clavipes
 Spider silk protein
 19-NOV-1999
 AAY40097;
 AAY40097 standard;
 Sequence
 skin and hair.
 Claim 3; Fig 1; 32pp; French.
 (OREA) L'OREAL
 11-FEB-1998;
 hormone; moisturizer; skin disorder; skin disorder.
 486
 614
 hormones, moisturizers or agents for treating disorders of the
 167
 Local
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 PTNSAALSSTISNVVSQIGAS
 1999-510729/43
 ptnsaalsstisnvvsqigas
 \tt grgglgggagaaaaggagggggggggsgasaasaasrlsspgassrvssavsnlvasg
 AAAGGAGOGGYGGLGSQGAGRGGLGGQGAG--AAAAAGGVGQGGLGG---QGAGQGA-GA
 GGQQMGRIRIRGYGGLGGQGAGQGAGAAAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAAA
 GLGSQGAGRGGLGGQGAGA--
 aaaggaggggygglgsqgagrgglggqgagaaaaaaggagggggggglgnqgagrgggga
 AAAAAGGAGQGGYGGLGSQGAGRGGSGGQGAGAAAAAAG---
 Similarity
 Conservative
 Garson
 (first
 AA;
 98FR-0001614
 98FR-0001614
 protein;
 spidroine major
 'n,
 74.0%;
 Arraudeau
 694
 5
 Score 1999; DB 20;
Pred. No. 2.1e-130;
5; Mismatches 10;
 ۲
 skin care; sunscreen;
 Indels 188;
 Length
 651;
 -GAGQGGYG
 have
 Gaps
 198
 166
 . 119
 673
 78
 65
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RESULT
AAR99055
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 This sequence represents a synthetic spider dragline variant polymer, pp-1B.9. The sequence of the Dp-1B.9 monomer is given in AAR99054. The polypeptide monomer is a variant based on a consensus sequence derived from the fibre forming regions of spider dragline protein,
 New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
 Spider; dragline protein; variant; monomer; polymer; fibre forming region; Spidroin 1; Nephila clavipes; DP; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope; surgical suture; implant; reinforcement; film; coating.
 Disclosure; Page 88-90;
 Fahnestock
 22-DEC-1994
 WO9429450-A2
 Spider dragline
 17-JAN-1997
 AAR99055
 AAR99055 standard;
 15-JUN-1993;
 15-JUN-1994;
 na (oana)
 614
 426
 498
 337
 438
 325
 378
 285
 318
 233
 199
 6
 GAGGLGGQGAGAAAAVGAGQGGYGGVGSGASAASAAAS 463
 1995-036479/05
 grgglggggagaaaaggaggggggggggasaasaaaa
 QGAGAAAAAAAAAGGVRQGGYGGLGSQGAGRGGQGAGAAAAAAAGGAGQGGTGGLGGQGV
 AAGGAGOGGYGG---OGAGQG-------GYGGLGSOGAGRGGLGGOGAGA 324
 AAAAGGAGQGGLG----GQGAGAAAAAAGGAGQGGYGGLGSQGAGR---GGQGAGA-AAA 284
 gsqgagrggegagaaaaaaggagqggygglggqgagqggygglgsqgagrgglggqgag-
 qgag----aaaaaaggvrqggygg1gsqgagrggqgagaaaaaaggaggggggggggggv
 aaavgagqeg1rgqgagqggygg1gsqgsgrgg1ggqgagaaaaaaggagqgg1ggqgag
 aaaaaaggaggggggglgnqgagrggggaaaaaggagggggggglgsqgagrggggagaaa
 aaggagqggygglgsqgagrgggagaaaaaaggagqrgygglgnqgagrgglggqgaga
 aaaaggagqgg1ggqgagqagaaaaaaggagqggygg1gsqgagrgg1ggqgagavaaa
 -----AAAAAAGGAGQGGYGGLGGQGAGQGGYGGLGSQGAGRGGLGGQGAGA
 glgsqgagrgglggqgagaaaaaaaggagqgglggqgagqgagasaaaaggagqggyggl
 PONT
 (first entry)
 93US-0077600
 94WO-US06689
 Œ
 NEMOURS & CO
 Protein;
 ------GGLGGQGAGAAAAAAGGAGQGGLGGQGAG
 -----AAAAAGGAGQ-----
 168pp;
 DP-18.9
the DP-1B.9 monomer is given in AAR99054.
a variant based on a consensus sequence
ming regions of spider dragline protein,
 606
 English.
 ₹
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 polymer
 317
 437
 613
 425
 557
 365
 497
 336
 377
 232
 258
```

AGAAAAAAGGAGQGGTGGLGGQGVGAGGLGGQGAGAAAAVGAGQGGYGGVGS

gqggygglgsqgagqggygglgsqgagrgglggqgagaaaaaaaggagqgglgsqgagqg

RQGGYGGLGSQGAGRG-----

606

401 554 382 494 329 435

GRGGQGAGAAAAAGGAGQGGYGG---QGAGQGGYGGLGSQGAGGGGGGGGGGGAGAAAAA

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 cc esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. The DNA sequence encoding the monomer may be used in the recombinant control of the variant protein in a recombinant host, e.g. E. coli credillus subtills. Synthetic analogues of DP1 were designed to mimic the repeating consensus sequence of the natural protein and the pattern conformatities of (1)-(5) below. In addition, it exhibits all of the regularities of (1)-(5) below. In addition, it exhibits a regularity of the natural sequence which is not shared by DP-1A, namely that a repeat in which both GYG and GRG are deleted is generally preceded by a repeat clacking the entire poly-alanine repeat, with one intervening repeat. The sequence of DP-1B matches the natural sequence more closely over can more extended segment than does DP-1A. The individual repeats differ creating the the poly-alanine sequence varies in length from 0.7 cc (1) the poly-alanine sequence varies in length from 0.7 cc (1) the surrounding sequence varies in length from 0.7 cc (3) aside from the poly-alanine sequence, deletions usually cc encompass integral multiples of three consecutive residues; (4) deletion of GYG is generally accompanied by deletion of GRG in the same sequence; and
 Matches 412;
 Query Match
Best Local Similarity
 The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
 Sequence
 deleted
 in
 residues.
 317
 186
 197
 159
 140
 106
 80
 21
 the same sequence; and (5) a repeat in which the entire poly-alanine sequence is leted is generally preceded by a repeat containing six alanine
 σ
 GGQQMGRIRI-----RGYGGLGGQGAGQGAGAAAAAAAAGGAGQGGYGGLGSQGAGRGGQG
gagrgglggggagaaaaaaaggagggglgsqgaggagaaaaaaggaggggggglgsqga
 GAGRGGLGGQGAG--AAAAAGGAGQGGLG----GQGAGAAAAAAGGAGQGGYGGLGSQGA
 aaaggagggggglgscgagcgagagaaaaaggagggggglgscgagggggggglgsc
 gglgsqgagqggygglgsqgagrgglggqgagaaaaaaggagqgglgsqgaggagaaa
 gglgsqgagqagaaaaaggagqggygglgsqgagr---ggqgagaaaaaaggagqggy
 GGLGGQGAGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGSGGQGAGAAAAAAG-----
 agaaaaaaggagqggygglgsqgaggggggggggagaaaaaaggagq
 AGAAAAAAG------GAGQGGYGGLGSQGAGRGGLGGQGAG--AAAAAGGVGQ 105
 -----GAGQGGYGGLGSQGAGRGGLGGQGAGA-----
 ggqgagaaaaaaaggagqgglgsqgagqgag-aaaaaaggagqggygglgsqgagrggqg
 Conservative
 Ä
 -----AAAAAAGGAGQGGYGGLGGQGAGQGGYGGLGSQ
 69.8%;
 ω
••
 Score 1883.5; DB 1
Pred. No. 1.7e-122;
 Mismatches
 16; Length 606;
 151;
 Gaps
 139
 316
 256
 60
 376
 272
 218
 185
 158
 79
 16;
```

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RESULT
AAY40102
• S
 В
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 В
 20
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 Query Match
Best Local S
Matches 412
 The present sequence represents a polymer of an analogue of the spider silk protein spidroine major 1. The protein improves the moisturizing/ softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active agencs that are generally difficult to administer, e.g. vitamins,
 Synthetic.
Nephila cl
 Cosmetic or dermatological composition containing spider for hair or skin care, in make-up or sunscreens
 Key
 Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscrehormone; moisturizer; skin disorder; skin disorder.
 AAY40102 standard; protein;
 Sequence
 hormones, moisturizers or agents for treating disorders of the skin and hair.
 Claim
 WPI; 1999-510729/43
 Philippe M,
 (OREA) L'OREAL
 11-FEB-1998;
 11-FEB-1998;
 13-AUG-1999
 FR2774588-A1
 Peptide
 Polymer of an
 19-NOV-1999
 AAY40102;
 159
 140
 106
 80
 61
 21
 7
 GGLGGQGAGQAAAAAAAGGAGQGGYGGLGSQGAGRGGSGGQGAGAAAAAAG------
 GGQQMGRIRI-----RGYGGLGGQGAGQGAGAGAAAAAAAGGAGQGGYGGLGSQGAGRGGQG 60
 gglgsqgagqaaaaaaggagqggygglgsqgagr--
 agaaaaaaggagggggglgsqgaggggggggggggggggagaaaaaaggagg 139
 AGAAAAAG----
 ggqgagaaaaaaaggagqgglgsqgagqag-aaaaaaggagqggygglgsqgagrggqg
 al Similarity
412; Conser
 clavipes.
 Fig
 606
 -GAGQGGYGGLGSQGAGRGGLGGQGAGA----
 69.8%; llarity 69.6%; Conservative
 Garson JC,
 6B;
 (first entry)
 analogue of spider silk protein spidroine major 1.
 A,
 98FR-0001614.
 98FR-0001614
 SA
 1..101
/note=
 32pp; French.
 Location/Qualifiers
 "monomer unit"
 Arraudeau
 -GAGQGGYGGLGSQGAGRGGLGGQGAG--AAAAAAGGYGQ 105
 606
 Score 1883.5; DB 20;
Pred. No. 1.7e-122;
3; Mismatches 26;
 ⋧
 -ggqgagaaaaaaggagqggy 196
 Indels
 sunscreen;
 Length 606;
 silk
 151;
 protein,
 Gaps
 79
 16;
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 Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens
 Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscrehormone; moisturizer; skin disorder; skin disorder.
 WPI;
 Philippe M,
 11-FEB-1998;
 11-FEB-1998;
 13-AUG-1999
 FR2774588-A1
 Peptide
 Nephila
 Synthetic
 Polymer of an analogue of spider silk protein spidroine major
 19-NOV-1999
 AAY40101;
 AAY40101 standard;
 (OREA) L'OREAL SA.
 555
 402
 495
 383
 436
 330
 377
 317
 219
 257
 197
 273
 œ
 GRGGQGAGAAAAAAGGAGQGGYGG---QGAGQGGYGGLGSQGAGRGGLGGQGAGAAAAAA
 1999-510729/43
 agaaaaaaggagqggygglgsqgagrggqga-gaaaaaaggagqggygglgs
 AGAAAAAAGGAGQGGTGGLGGQGVGAGGLGGQGGAGAAAAVGAGQGGYGGVGS
 aaggagqgglgsqgaggagaaaaaaggagqggygglgsqgagrg-gqgagaaaaaagga 494
 gagrgglggqgagaaaaaaaggagqgglgsqgagqgagaaaaaaggagqggygglgsqga
 GAGRGGLGGQGAG--AAAAAAGGAGQGGLG----GQGAGAAAAAAGGAGQGGYGGLGSQGA
 aaaggagggggglgsqgagrgggggagaaaaaaggagggggggglgsqgaggggggglgsq
 gglgsqgagqggygglgsqgagrgglggggagaaaaaaaggagqgglgsqgagqagaaa
 gqggygglgsqgaggggglgsqgagrgglggagaaaaaaaggagqgglgsqgagqg
 grggggagaaaaaaggagggygglgsqgaggggygglgsqgagrgglgggag-aaaaa
 RQGGYGGLGSQGAGRG-----
 clavipes
 Garson JC,
 (first entry)
 98FR-0001614
 98FR-0001614
 Location/Qualifiers
 /note-
 protein;
 "monomer unit"
 Arraudeau
 606
 ₽
 JP;
 sunscreen;
 605
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 401
 435
 376
 272
 316
 256
 554
```

The present sequence represents a polymer of an analogue of the spider silk protein spidroine major 1. The protein improves the moisturizing/ softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make-up or sunscreens.

Claim 8;

Fig

5B; 32pp; French.

```
RRESULT
AAR9907
ID AAR9
XX AAR9
AC AAR9
XX T7-J
DT 17-J
DT 17-J
XX Spid
KW Spid
KW Spid
KW Fibu
KW CP-J
KW CP-J
XX Synt
XX WO94
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 Matches 411;
 Query Match
Best Local
 As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins, hormones, moisturizers or agents for treating disorders of the skin and hair.
 Spider; dragline protein; variant; monomer; polymer; fibre forming region; Spidroin 1; Nephila clavipes; DP1; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; cloth
 W09429450-A2
 Synthetic
 Spider dragline
 17-JAN-1997
 AAR99057 standard;
 Sequence
 AAR99057;
 557
 402
 497
 383
 438
 330
 379
 273
 319
 219
 259
 186
 199
 159
 142
 106
 82
 61
 Local Similarity
 23
 σ
 9
 GRGGQGAGAAAAAAGGAGQGGYGG---QGAGQGGYGGLGSQGAGRGGLGGQGAGAAAAA 329
 GGQQMGRIRI-----RGYGGLGGQGAGAQGAGAAAAAAAGGAGQGGYGGLGSQGAGRGGQG
 AGAAAAAAGGAGQGGTGGLGGQGVGAGGLGGQGAGAAAAVGAGQGGYGGVG 452
 gagrgglggggagaaaaaaaggagggglgsggaggagaaaaaaggaggggggglgsqga
 GAGRGGLGGQGAG--AAAAAGGAGQGGLG----GQGAGAAAAAAGGAGQGGYGGLGSQGA
 aaaaggagqggygglgsqgagragagaaaaaaggagqggygglgsqgagqggygglgsq
 GGLGGQGAGQGAGAAAAAAGGAGGGGYGGLGSQGAGRGGGGGGGAGAAAAAAG------
 AGAAAAAAG -----GAGQGGYGGLGSQGAGGLGGQGAG--AAAAAGGGGQ 105
 agaaaaaaggagqggygglgsqgagqga-gaaaaaaggagqggygglg
 9q99y9g19sq9a9q9gy9g19sq9a9r9g19gqgagaaaaaaaggagqgg1gsqgagqg
 RQGGYGGLGSQGAGRG------
 aaggagqgglgsqgagqagaaaaaaggagqggygglgsqgagrg-gqgagaaaaaagga 496
 grggqgagaaaaaaggagqggygglgsqgagqggygglgsqgagrgglggqgag-aaaaa
 gglgsqgagqggygglgsqgagrgglgggagaaaaaaaggagqgglgsqgagqgagaaa
 -----GAGQGGYGGLGSQGAGRGGLGGQGAGA------
 gglgsqgagqagaaaaaaggagqggygglgsqgagr---ggqgagaaaaaaggagqggy 198
 agaaaaaaggagggygglgsqgagggggglgsqgagrgglggggagaaaaaaggagg 141
 ggqgagaaaaaaaggagqgglgsqgagqgag-aaaaaaggagqggygglgsqgagrggqg
 606 AA;
 Conservative
 (first entry)
 ------AAAAAAGGAGQGGYGGLGGQGAGQGGYGGLGSQ 218
 Protein; 604
 69.6%;
 implant;
 DP-18.16 polymer.
 Score 1879.5;
Pred. No. 3.3e.
3; Mismatches
 ω
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 reinforcement; film; coating
 . 3e-1
 DB 20;
 Indels 151;
 Length
 - ဝင္ထင္ပ
 Gaps
 378
 556
 401
 437
 272
 318
 258
 185
 81
 60
 16;
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 derived from the fibre forming regions of spider dragline protein, CC esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. The CC DNA sequence encoding the monomer may be used in the recombinant CC DNA sequence encoding the monomer may be used in the recombinant CC or Bacillus subtilis. Synthetic analogues of DP1 were designed to mimic CC the repeating consensus sequence of the natural protein and the pattern CC of variation among individual repeats. This monomer exhibits all of the regularities of (1)-(5) below. In addition, it exhibits a regularity of the natural sequence which is not shared by DP-1A, namely that a repeat CC the natural sequence which is not shared by DP-1A, namely that a repeat CC in which both GYG and GRG are deleted is generally preceded by a repeat CC a more extended segment than does DP-1A. The individual repeats differ CC a more extended segment than does DP-1A. The individual repeats differ CC (1) the poly-alanine sequence waries in length from 0-7 (2) when the entire poly-alanine sequence is deleted, So also is the surrounding sequence encompassing AGRGGLGCGGAGAGGGGCC (3) aside from the poly-alanine sequence, deletions usually CC encompass integral multiples of three consecutive residues; (4) deletion of GYG is generally accompanied by deletion of GRG in the same sequence; and
 Query Match
 Matches 411;
 Best Local Similarity
 This sequence represents a synthetic spider dragline variant polymopp-1B.16. The sequence of the DP-1B.16 monomer is given in AAR990. The polypeptide monomer is a variant based on a consensus sequence
 Sequence
 The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
 Disclosure; Page 106-108; 168pp; English.
 etc., also related DNA, vectors and transformed cells
 New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement
 WPI; 1995-036479/05
 15-JUN-1994;
 22-DEC-1994
 deleted is
 DUPO) DU
 106 GGLGGQGAGQAAAAAAAGGAGQGGYGGLGSQGAGRGGSGGQGAGAAAAAAG-----
189 AAAGGAGQGGYGGLG
 23
 61 AGAAAAAG-----
 the same sequence; and
(5) a repeat in which the entire poly-alanine sequence is
leted is generally preceded by a repeat containing six alanine
 6 GGQQMGRIRI-----RGYGGLGGQGAGQGAGAAAAAAAGGAGQGGYGGLGSQGAGRGGQG
 ggqgagaaaaaaaggagqgglgsqgagqgag-aaaaaaaggagqggygglgsqgagrggqg
 gglgsqgagqggygglgsqgagrgglggqgagaaaaaaaggagqgglgsqgagqagaaa
 agaaaaaaggagggygglgsqgagggygglgsqgagrgglggggagaaaaaaggagq
 gglgsqgagqaaaaaaggagqggygglgsqgagr--
 -GAGQGGYGGLGSQGAGRGGLGGQGAGA----
 604 AA;
 Conservative
 94WO-US06689
 DE
 NEMOURS &
 -----GAGQGGYGGLGSQGAGRGGLGGQGAG--AAAAAAGGVGQ
 69.3%;
69.8%;
 ω
--
 Score 1871.5;
Pred. No. 1.26
 ဗ
 Mismatches
 (T)
 5; DB 16;
.2e-121;
 -ggqgagaaaaaaggagqggy 198
 gline variant polymer, is given in AAR99056.
 GQGAGQGGYGGLGSQGA
 Indels 149;
 Length 604;
 AAA
 Gaps
 258
 188
 105
 158
 141
 81
 60
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 9053
 This sequence represents a synthetic spider dragline variant polymer, DP-1A.9. The sequence of the DP-1A.9 monomer is given in AAR99052. The polypeptide monomer is a variant based on a consensus sequence derived from the fibre forming regions of spider dragline protein, esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. DNA sequence encoding the monomer may be used in the recombinant production of the variant protein in a recombinant host, e.g. E. coli or Bacillus subtilis. Synthetic analogues of DP1 were designed to mimic the repeating consensus sequence of the natural protein and the pattern of variation among individual repeats. DP-1A analogues are composed of a tandemly repeated 101 amino acid monomer which comprises four repeats which differ from the consensus sequence given in AAW06201,
 Spider; dragline protein; variant; monomer; polymer; fibre forming region; Spidroin 1; Nephila clavipes; DP1; mimic; DP-lA analogue; fibre; high tensile strength; elasticity; cloth rope; surgical suture; implant; reinforcement; film; coating.
 17-JAN-1997
 AAR99053 standard; Protein; 606
 New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
 15-JUN-1993;
 15-JUN-1994;
 Spider dragline variant, DP-1A.9 polymer.
 Disclosure;
 WPI; 1995-036479/05
 (DUPO) DU
 WO9429450-A2
 Synthetic
 497
 438
 404
 10
 GGQGAGAAAAAAGGAGQGGYGG----QGAGQGGYGGLGSQGAGGGGGGGGAGAAAAAAAAA
 GRGGLGGQGAG---AAAAAGGAGQGGLG----GQGAGAAAAAAGGAGQGGYGGLGSQGAGR 274
 aaaggagqggygglgsqgagrggqgagaaaaaaggagggygglgsgagqggygglgsqga
 ggygglgsqgagqggygglgsqgagrgglggqgagaaaaaaaggagqgglgsqgagqgag
 ggagqgglgsqgagqaaaaaaggagqggygglgsqgagrg-gqgagaaaaaaggagq
 grgglggggagaaaaaaaggaggglgsqgaggagaaaaaaggaggggggglgsqgagr
 aaaaaaggagqggygglgsqgagrggqga-gaaaaaaggagqggygglg
 AAAAAAGGAGQGGTGGLGGQGVGAGGLGGQGAGAAAAVGAGQGGYGGVG
 GGYGGLGSQGAGRG-----
 PONT
 Page 85-87; 168pp; English.
 (first entry)
 9308-0077600
 94WO-US06689.
 B
 NEMOURS & CO
 (F)
 604
 452
 clothing;
 GOGAG
 496
 331
 318
 556
 403
 437
 378
 384
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RESULT AAY40100

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AAY40100;

100 AAY40100

standard;

protein;

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19-NOV-1999

(first

entry)

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 Query Match
Best Local S
Matches 409
 according to the pattern (1)-(5) given below. This 101 amino acid monomer is repeated 1-16 times in a series of analogue proteins. The individual repeats differ from the consensus according to the pattern: (1) the poly-alanine sequence varies in length from 0-7 residues; (2) when the entire poly-alanine sequence is deleted, so also is the surrounding sequence encompassing AGRGGIGGGGARAGG; (3) aside from the poly-alanine sequence, deletions usually encompass integral multiples of three consecutive residues; (4) deletion of GVG is generally accompanied by deletion of GRG in the same sequence; and
 The proteins may be used to produce fibres of high tenselasticity, suitable for clothing, rope, surgical suture for implants, plastic reinforcements, films, coatings,
 deleted is
 Sequence
 450
 506
 394
 446
 389
 297
 335
 278
 218
 157
 158
 107
 566
 86
 49
 38
 Local Similarity
 σ
 AGQGGLGGQGAG-AAAAAAGGAGQGGYGGLGSQGAGGGGGGAGAAAAAAAGGAGQGGYGG-
 glgsqgagqgagaaaaaaggagqggygglgsqgagqggygglgsqgagrggqgagaaaaa
 LGSQGAGRGGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGLGGQGAG--AAAAAAGGYGQG
 ggqgagaaaaaaaggagqgglgsqgaggagaaaaaaggagqggygglgsqgagqggygg
 GGQQMGRIRI-----GAGQGGGGGGAGAAAAAAAG-----GAGQGGYGG
qgagqgagaaaaaa
 agaaaaaaaggaggglgsqgagqgagaaaaaaggaggggggglgsqgagqggygglgsq
 gagqggygglgsqgagqggygglgsqgagr---ggqgagaaaaaaggagqggygglgsqg
 GAGQGGYGGLGGQGAGQGGYGGLGSQGAGRGGLGGQGAGAAAAAG------G
 aggagqggygglgsqgagrgglggqgagaaaaaaaggagqgglgsqgagqgagaaaaaag
 lgsqgagrggggagaaaaaaggagggggglgsqgagrgglgggggagaaaaaaggaggg
 409;
 GAGRGGQGAGAAAAAAGGAGQGGTGGLGGQGVGAGGLGGQGAGAAAAV---GAGQGGYG-
 AG-AAAAAAGGAGQGGLGGQGAGQGAGAAAAAAAAAA :-----AGGVRQGGYGGLGSQ
 agrgglggggagaaaaaaaggagg---gglgsqga---gqgagaaaaaaggagqggyggl
 -GVGSGASAASAAA
 gagrggggagaaaaaaggaggggggglgsggagrgglggggagaaaaaaggagggglgs
 generally
 606 AA;
 Conservative
 579
 462
 68.8%;
73.8%;
 preceded by a repeat containing
 5;
 Score 1858.5; DB Pred. No. 9.2e-121
 Mismatches
 fibres of high tensile strength
 16;
 h tensile strength and sutures, biomaterials
 Indels 109;
 Length 606
 six alanine
 -----AAAAAAG
 etc.
 Gaps
 449
 445
 156
 106
 97
 48
 505
 393
 343
 388
 334
 238
 277
 192
 217
 157
 296
 18;
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 Query Match
Best Local
 Matches
 The present sequence represents a polymer of an analogue of the spider silk protein spidrolne major 1. The protein improves the moisturizing/softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins,
 Cosmetic or dermatolog for hair or skin care,
 Claim 8;
 11-FEB-1998;
 Synthetic
 Sequence
 hormones, moisturizers or agents for treating disorders of the skin and hair.
 WPI; 1999-510729/43
 Philippe M,
 (OREA) L'OREAL SA
 11-FEB-1998;
 13-AUG-1999
 FR2774588-A1
 Peptide
 Key
 Nephila clavipes
 Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscreen; hormone; moisturizer; skin disorder; skin disorder.
 Polymer
 335
 278
 193
 218
 157
 158
 239
 107
 98
 49
 38
 6
 AGQGGLGGQGAG-AAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAAAAAAGGAGQGGYGG-
 gagqggygglgsqgagqggygglgsqgagr---ggqgagaaaaaaggagqggygglgsqg
 aggagqggygg1gsqgagrgg1ggqgagaaaaaaggagqgg1gsqgagagaaaaag
 AGGAGQGGYGGLGSQGAGRGGLGGQGAGA-----
 glgsqgagqgagaaaaaggagqggygglgsqgagqggygglgsqgagagaaaa
 LGSQGAGRGGQGAGAAAAAGGAGQGGYGGLGSQGAGRGGLGGQGAG--AAAAAGGYGQG 106
 99qgagaaaaaaaggagqgglgsqgagqagaaaaaaaggagqggygglgsqgagqggygg
agrgglggqgagaaaaaaggagg---gglgsqga---gggagaaaaaaggagqggyggl
 Similarity
 of an analogue of spider silk protein spidroine major
 F1g
 606
 dermatological composition containing spider silk protein, skin care, in make-up or sunscreens -
 Conservative
 Garson JC,
 4B;
 ₹
 98FR-0001614
 98FR-0001614
 Location/Qualifiers
1..101
 32pp; French.
 68.8%;
73.8%;
 "monomer unit"
 Arraudeau
 ٠.
ب
 Score 1858.5; DB 2
Pred. No. 9.2e-121;
 Mismatches
 DB 20;
 Indels
 Length 606
 -GSGGQGAGAAAAA 156
 -----AAAAAAG 192
 109;
 Gaps
 157
 296
 334
 277
 217
 97
 238
 18;
```

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RESULT :
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 This sequence represents the product of cDNA clone, pMISS1, encoding the orb web spider minor ampullate silk protein MiSP1 has been identified and sequenced. Repeat unit peptides of MiSP1 may form part of a larger polypeptide with an amino terminus (see AAR80184-85) and a carboxy terminus (see AAR80186-89). Repeat unit peptides make up and a carboxy terminus (see AAR80186-89). Repeat unit peptides make up spider silk proteins (spidroins) which in turn aggregate to form the silk fibres have high tensile strength and significant elasticity. An isolated cDNA clone of a silk protein encoding sequence is of use to produce the protein at high yields
 Polypeptide(s) comprising repeated unit amino acid sequences, cDNAs - derived from minor ampullate spider silk proteins and to form spider silk fibres
 Claim 2; Fig 1; 86pp; English.
 WPI; 1995-336970/43
N-PSDB; AAQ98470.
 Colgin M,
 Key Location/Qualifiers Misc-difference 272..285
 Spider silk;
 pMISS1 MiSP spider
 01-MAY-1996
 AAR80168;
 AAR80168 standard; Protein;
 (UYWY-) UNIV WYOMING
 14-MAR-1994;
 14-MAR-1995;
 W09525165-A1
 Nephila clavipes.
 spidroin; MiSP; orb web
 566
 450
 506
 446
 344
 389
 394
 297 --QGAGQGGYGGLGSQGAGRAGGLGGQGAGAAAAA-AAG-------GAGQGGLGGQG
 12
 GAGRGGQGAGAAAAAAGGAGQGGTGGLGGQGVGAGGLGGQGAGAAAAV---GAGQGGYG- 449
 qgagqgagaaaaaa 579
 -GVGSGASAASAAA 462
 AG-AAAAAAGGAGQGGLGGQGAGQGAGAAAAAAAAA---
 gsqgagqggygglgsqgagr----ggqgagaaaaaaggagqggygglgsqgagrgglggqg
 gagrggqgagaaaaaaggagqggygglgsqgagrgglggqgagaaaaaaaggagqgglgs
 agaaaaaaaggagggglgsqgagqgagaaaaaaggaggggggglgsqgagggggggglgsq
 Lewis RV
 repeat unit; consensus; minor ampullate silk protein;
 (first entry)
 94US-0209747
 95WO-US03139
 /note-
 DNA
 silk protein insert product
 technology.
 "represented as
to a highly com
AAQ98470 which
 spider; dragline
 831
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 as indeterminate,
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Sequence

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RRESULT 1
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 Query Match
Best Local Similarity
 Matches 343;
 Spider silk protein; spidroine minor 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscre hormone; moisturizer; skin disorder; skin disorder.
 Spider silk protein spidroine minor 1.
 AAY40099 standard; protein;
 137
 150
 Nephila clavipes
 19-NOV-1999
 194
 739
 93
 49
 93
 13
 ygagagagaaaaagagsggaggygrgagagagagaaagagagagsygggggggagagaaaa
 aagaggygrg---aggyggggggggagagagaaaaagagagggaggygrgagagaaaagag
 ASMTGGQQMGRIRIRGYGGLGGQGAGQGAGAAAAAAAGGAGQGGYG------
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 ----SQGAGRGGLGGQ-----GAGAAAAAAG------
 ---grgagaggygggggggagagagaaaagagggggdkeiacwsrcrytvasttsrls
 GLGGQGVGAGGLGGQ------GAGAAAAVGAGQGGYGGVGSGA-----SAASAAASRLS
 AAAAGGAGQGGYG------GQGAGQGGYGGLGSQGAG------
 gagagagaaaaaatgaggaggygrgagagagaaagagagtggagyggggggggagagaaa
 ----GAGAAAAAAGGA-GQGGYG------GLGSQGAGRGGQ------GAGAA
 saeassrissaastlvsggylntaalpsvisdlfaqvgasspvirgrs-liqvll
 SPQASSRVSSAVSNLVASGPTNSAALSSTISNVVSQIGASNPGLSGCDVLIQALL 521
 aggygrgagagaaagagaaagagagaggygggggggga----gagaaaaagagagrggy-
 LGGQGAGQGAGAAAAAAAAAAGGVRQGGYGGLGSQGAGRGGQGAGAAAAAAAGGAGQGGTG
 agaggaagysrggrag-aagagagaaaagagaggygggggygagagagaaaaagagsgg
 ------SQGAGRGGSG--GQGAGAAAAAAGGAGQGGYGGLG------
 -GAGAAAAAGGVGQGGLGGQGAGQGAGAAAAAAAGGAGQGGYGGLG------
 Conservative
 (first entry)
 49.8%;
 19;
 615
 Score 1344; DB 16; Pred. No. 3.2e-85;
 Mismatches 143;
 Length
 Indels
 sunscreen;
 210;
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 Gaps
 209
 448
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 Matches
 Query Match
Best Local :
 The present sequence represents the natural spider silk protein spidroine minor 1. The protein improves the moisturizing/softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins, hormones, moisturizers or agents for treating disorders of the skin and hair.
 WPI;
 Claim 7; Fig 3; 32pp; French
 Cosmetic or dermatological for hair or skin care, in n
 Philippe M,
 11-FEB-1998;
 Sequence
 (OREA) L'OREAL
 359
 299
 221
 239
 137
 119
 273
 93
 59
 49 LGSQGAGRGGQ-----GAGAAAAAGGAGQGGYGGLG-----SQGAGRGGLGGQ--
 N
 1999-510729/43
gsggaggygrgagagaaagagaaagagagaggyggggygagagaaaaagagagrggygr 590
 GRGGQGAGAAAAAAGGAGQGGYG---GQGAGQGGYGGLGSQGAGRGGLGGQGAGAAAAAA
 GRGGLGGQ-----GAGA-AAAAGGAGQGGLG--GQGAGAAAAAAGGAGQGGYGGLGSQGA
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 ygagagagaaaaaagagsggaggygrgagagagaaagagagagsygggggggggagagagaa 178
 GQGGTGGLG----
 ---gagagaaaaatgaggaggygrgagagagaaagagagtggagyggggggggagagaaa
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 ---SQGAGRGGIGGQ-----GAGAAAAAAGGAGQGGYGGIGGQGGAGQGGYGGIG-SQGA
 SQGAGRGGSGGQGAGA-------AAAAAGGAGQGGYGGLG-----
 AAGGAGQGGIG-GQGAGAAAAAAGGA--------GQGGIGGQGAGGGAGAAAAAA 375
 agaggaagysrggragaagagagaaagagagaggyggggggga----
 309;
 Similarity 49.4
09; Conservative
 615 AA;
 Garson
 98FR-0001614
 98FR-0001614
 45.7%; Score 1234; DB 20; 49.4%; Pred. No. 8.8e-78;
 ر
کر
 ical composition containing spider silk protein, in make-up or sunscreens
 Arraudeau
 ----GQGVGAGGLGGQ-----GAGAAAAVGA-----
 12; Mismatches
 GVRQGGYGGLGSQGAGRGGQGAGAAAAAAGGA 412
 Indels
 Length
 -gagagaaaaaga
 615;
 174;
 Gaps
 329
 475
 136
 92
 48
 415
 358
 298
 169
 530
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RRESULT 1
AAR11
XX AAR11
XX AAR1
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DT 18-A
XX POT 18-A
XX EP45
XX EP45
XX UPH
PH 18-A
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 Query Match
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 Matches
 The spider silk protein contains repeat regions comprising an amorphous region which can form an alpha-helix when stretched and a region which can form betted sheets. Removal of the poly-(Ala) segments results in a silk having lower elasticity. It is envisaged that derivatives of the silk protein could be produced having different tensile strength or elasticity than the natural protein by altering the ratio of different amino acids.
 DNA encoding spider silk protein-1 and 2 and variants - isolated from Nephila clavipes, for prodn. of spider silk protein and fibres having desired characteristics
 N.clavipes dragline silk protein-2.
 Sequence
 Claim 16; Page 30; 48pp; English.
 N-PSDB; AAQ14184.
 WPI; 1991-312199/43.
 20-APR-1990;
 18-APR-1991;
 23-OCT-1991.
 Nephilia clavipes.
 protein superfibre;
 15-JAN-1992
 AAR14309;
 AAR14309 standard;
 Lewis RV,
 (UYWY-) UNIV OF WYOMING.
 444
 172
 158
 123
 104
 591
 Local Similarity
 63
 57
 17
 14
 w
 GYG----GLGGQGAGQ----GAG-AAAAAAAAGGAGQGGYG------GLGSQGAGR--
 GGAGQ---GGYG---GLGSQGAGRGGLGGQGAGAAAAAAAAAGGAGQGGYGGLGGQGAGQG
 gagaggyggggygagagagaaaa
sgqqgpggygpgq------qgpgygpgqqgpggygpgqqgpsgpgsaaaaaaa
 -GQGGLGGQGAGQGAGAAAAAAGGAGQGGYG----GLGSQGAGRGGSGGQG-AGAAAAAA 157
 pgqqgpsgpgsaaaaaagsgqqgpggygprqqgpggygqgqqgpsgpgsaaaasaasae
 gygpgqqgpgqgpgqqqpsgpgsaaaaaaaaagpggygpgqqgpggygpgqqgpgryg
 313;
 -GGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGLG-GQ----GAGAAAAAGGV----
 -GQGGYGGVGSGASAASAAAS
 Xu M, Hinman
 595 AA;
 Conservative
 (first
 90US-0511792
 91EP-0106217
 Protein;
 major ampullate silk; orb web spider.
 entry)
 42.48;
51.18;
 25;
 595
 Score 1144;
Pred. No. 1
 615
 463
 Mismatches
 ₿
 1.3e-71
 DB 12;
 139;
 Indels 136;
 Length 595;
 Gaps
 103
 62
 56
 122
 171
 231
 210
 30;
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RESULT 15

AAW53347

ID AAW533

AC AAW533

XX AAW533

XX Spide

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 15-APR-1991;
20-APR-1990;
04-OCT-1994;
19-APR-1995;
 Recombinant spider silk proteins – useful for making fibres
 19-APR-1995;
 17-MAR-1998
 US5728810-A
 Nephila clavipes
 Spider; Nephila clavipes; silk protein; tandem repeat; fibre; dragline;
 Nephila clavipes spider silk protein
 06-JUL-1998
 AAW53347
 AAW53347 standard;
 (UYWY-) UNIV WYOMING
 520
 403
 576 pglsgcdvligal 588
 448
 460
 408
 359
 343
 316
 286
 508 PGLSGCDVLIQAL 520
 211
 1998-270437/24.
DB; AAV23250.
 yg----pgsqasaaasrlaspdsgarvasavsnlvssgptssaalssvisnavsqigasn
 YGGVGSGASAASAASRLSSPQASSRVSSAVSNLVASGPTNSAALSSTISNVVSQIGASN
 aaasagpggygpaqqgpsgpgiaasaasagpggygpaqqgpagygpgsavaasagagsag
 AAGGAGQGGTG----GLGGQGV------GAGGLG------GQGAGAAAAVGAGQGG
 pggyapgqqgpsgpgsasaaaaaaag--pggygp-gqqgpggyapgqqgpsgpgsaaaa
 LGGQGAGQ----RGGAAAAAAAAAAAGGVRQGGYGGLGSQGAG-----RGGQGAG-AAAA
 gpggygpgsasaaaaaagpgqqgpggygpgqqgpsgpgsasaaaaaaagpggygpgqqg
 GLGGQGAGAAAAAAAGGAGQGGLGGQGAG------AAAAAAG---
 ggygpgqqgpggygpgqqgpsgagsaaaaaagpgqqglggygpgqgpgg---ygpgqq
 GGYG----GLGSQGAG-RGGQGAG-AAAAAAGGAGQGGYGGQGAGQGGYGGLGSQGAGRG
 GYGGLGSQGAGRGGLGGQGAGAAAAAGGAGQGGLGGQGAG-----AAAAAAAGGAGQ
 ۲.
 MB,
 tensile strength; elasticity
 Column 37-42; 68pp; English.
 Lewis RV,
 (first entry)
 -gpgqqglsgpgsaaaaaaagpgqqgpggygpgqqgpsgpgsaaaaaaaagp
 91US-0684819.
90US-0511792.
94US-0317844.
95US-0425069.
 95US-0425069
 Protein;
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 X
 595
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 -GAGQGG
 507
 342
 459
 402
 575
 519
 447
 407
 285
 358
 261
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The present sequence represents a spider silk protein from the present invention. Spider silk proteins, and peptide fragments within the proteins, can be produced and purified independently and can then be mixed and made into fibres that have higher tensile strengths and elasticity than naturally occurring fibres. The fibres can be used in mixed composites. The invention allows the two naturally occurring Nephila clavipes silk proteins to be produced independently so that

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Search completed: July Job time: 443 sec
 Query Match 42.4%; Score 1144; DB 19; Best Local Similarity 51.1%; Pred. No. 1.3e-71; Matches 313; Conservative 25; Mismatches 139;
 they can later be combined to form silk fibres of high tensile strength and elasticity.
 Sequence
 172 sgpgqqgpggygpgqgpggygpgqqppsgpgsaaaaaaasgpgqqgpggygpgqqgpg 231
 158
 123 вдаддрддудрда------адрддудрдадрддудрдадрддрддрздрааааааааа 171
 104 -GQGGLGGQGAGQGAGAAAAAAGGAGQGGYG----GLGSQGAGRGGSGGQG-AGAAAAAA 157
 232 gy-----gpgqqglsgpgsaaaaaagpgqqgpggygpgqqgpsgpgsaaaaaaaagp
 211 GYGGLGSQGAGRGGLGGQGAAAAAAGGAGQGGLGGQGAG------AAAAAAGGAGQ 261
 508 PGLSGCDVLIQAL 520
 460
 403 pggyapgqqgpsgpgsasaaaaaaag--pggygp-gqqgpggyapgqqgpsgpgsaaaa
 359
 316 GLGGQGAGAAAAAAAGGAGQGGLGGQGAG-------AAAAAAG----GAGQGG
 17 GYG-----GLGGQGAGQ-----GAG-AAAAAAAAGGAGQGGYG--------GLGSQGAGR-- 56
 63 pgqqgpsgpgsaaaaaagsgqqgpggygprqqgpggyggqqqppsgpqsaaaasaaasaa 122
 57 ----GGQGAGAAAAAGGAGQGGYGGLGSQGAGRGGLG-GQ----GAGAAAAAGGV---- 103
 GGAGQ---GGYG----GLGSQGAGRGGLGGQGAGAAAAAAAGGAGQGGYGGLGGQGAGQG 210
 дудрэддэрдэүдрэддэрээрдзаавааааааррэдудрэддэрэдуэрэддэрэгүд 62
 pglsgcdvligal 588
 aaasagpggygpaqqgpsgpg1aasaasagpggygpaqqgpagygpgsavaasagagsag
 AAGGAGGGGTG----GLGGGGV------GAGGLG-----GGGAGAAAAAVGAGQGG 447
 LGGQGAGQ----GAGAAAAAAAAAAGGVRQGGYGGLGSQGAG------RGGQGAG-AAAA 407
 595 AA;
 ω
 2001, 14:58:13
 Length
 Indels 136; Gaps
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Run

95:

OM protein -

Title: Perfect score:

sequence sequence

88, Appl 89, Appl 54, Appl 54, Appl 11, Appl 11, Appl 11, Appl 16, Appl 16, Appl 59, Appl 59, Appl 59, Appl 59, Appl 48, Appl 48, Appl

Sequence

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
 Total number of hits satisfying chosen parameters:
 d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
 protein search, using
 length:
 Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
 Query
Match
 BLOSUM62
Gapop 10.0 ,
 July 3, 2001, 14:56:41; Search time 48.42 Seconds (without alignments) 219.669 Million cell updates/sec
 US-09-490-291-8
2700
 193259 seqs, 20144635 residues
 1 MASMTGGQQMGRIRIRGYGG.....
 GenCore version
Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
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 Gapext 0.5
 US-09-034-177-3
US-08-317-644B-2
US-08-3137-644B-2
US-08-209-747-2
US-08-425-069-2
US-08-425-069-4
US-08-317-644B-4
US-08-175-155-29
US-08-477-509B-64
US-08-478-029A-31
US-08-478-029A-36
 summaries
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 SUMMARIES
 Compugen Ltd
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Sequence 41, Appli
Sequence 36, Appli
 Description
 CLONE:
US-09-034-177-3
 RESULT 1
US-09-034-177-3
 Sequence 3, Application US/09034177
Patent No. 6127146
GENERAL INFORMATION:
 Query Match
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 747 amino acid
 FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-5555
 LENGTH: 747 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 1174414
 APPLICATION NUMBER: US/
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
 APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN FIBROUS PROTEIN
NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 STREET: 3174 POIT
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
 TELEFAX: 650-845-4166
 ADDRESSEE:
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 PCT-US94-07776-16
US-08-4477-509B-94
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US-08-478-029A-48
 US-08-482-085B-88
US-08-477-09B-99
US-08-477-09B-99
US-08-175-155-54
US-09-010-928B-28
US-09-010-928B-2
US-08-089-662-11
US-08-587-333-18
 PF-0486
 Score 2273;
 ALIGNMENTS
 DB
 Length 747;
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Result

Score

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2222222111111111 22222221111111111 2654321098

1343.5 1344.5 1144 1144 1144 1972 972 972 972 972 962.5 962.5 962.5 962.5 962.5 962.5 962.5 962.5 962.5 962.5

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US-08-425-069-2
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Matches
 Sequence 2, Application US/08425069 Patent No. 5728810
 STREET: 301 No. 5728810th Washington Street CITY: Falls Church STATE: Virginia COUNTRY: U.S.A.
ZIP: 22046
 GENERAL INFORMATION:
 APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Xu, Ming
APPLICANT: Xu, Ming
APPLICANT: Yu, Ming
APPLICANT: Yu, Ming
APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 199
 139
 498
 438
 318
 233
 259
 167
 186
 120
 79
 22
 Local Similarity
 σ
 PTNSAALSSTISNVVSQIGASNPGLSGCDVLIQALL 521
 AAAAGGAGQGGLG----GQGAGAAAAAAAGGAGQGGYGGLGSQGAGR----GGQGAGA-AAA
 GSQGAGRGGEGAGAAAAAAGGAGQGGYGGLGGQGAGQGGYGGLGSQGAGRGGLGGQGAG-
 AAAAAGGAGQGGYGGLGSQGAGRGGSGGGGAGAAAAAAG-------
 AAAGGAGQGGYGGLGSQGAGRGGLGGQGAG--AAAAAGGVGQGGLGG---QGAGQGA-GA 119
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 GLGSQGAGRGGLGGQGAGA-----
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 GRGGLGGQGAGAAAAGGAGQGGYGGVGSGASAASAASRLSSPQASSRVSSAVSNLVASG
 {\tt GAGGLGGQGAGAAAAVGAGQGGYGGVGSGASAASAAASRLSSPQASSRVSSAVSNLVASG}
 -----AAAAAAGGAGQGGYGGLGGQGAGQGGYGGLGSQGAGRGGLGGQGAGA
 AAAAAAGGAGQGGYGGLGNQGAGRGGQGAAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAAA 497
 AA-----
 Conservative
 ------AAAAAGGAGQ-----
 71.0%;
 disk
 Pred.
 ed. No. 3.8e-160;
Mismatches 10;
 Indels
 -GAGQGGYG
 188;
 Gaps
 166
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 437
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 Matches
 Query Match
Best Local 9
 TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acid
TYPE: amino acid
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,069
FILLING DATE: 19-APR-1995
 NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald
 MOLECULE TYPE: protein
 199
 486
 366
 337
 438
 325
 378
 285
 233
 259
 186
 167
 139
 120
 LENGTH: 718 amino acids TYPE: amino acid TOPOLOGY: linear
 79
 66
 TELEFAX: (703) 205-8050
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 479;
 Similarity
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 81.3%;
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 506
 4;
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 Length
 Indels 188;

 Gaps
 138
 485
 425
 365
 497
 336
 437
 324
 377
 284
 317
 198
 673
 613
 557
 258
 185
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674 PTNSAALSSTISNVVSQIGAS 694

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OB/317,844B
FILING DATE: O4-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT., Gerald M
REGISTRATION NUMBER: 128,977
REFERENCE/DOCKET NUMBER: 1447-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
TOPOLOGY: linear
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 RESULT 3
US-08-317-844B-2
 US-08-317-844B-2
 Query Match 81.3%; Score 2196; DB 2; Best Local Similarity 70.3%; Pred. No. 1.7e-154; Matches 479; Conservative 4; Mismatches 10;
 Sequence 2, Application US/08317844B Patent No. 5989894
 GENERAL INFORMATION:
APPLICANT: Lewis,
APPLICANT: Xu, Mi
 TOPOLOGY: linear MOLECULE TYPE: protein
 APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
 STREET: 301 No. 598:
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22046
 186
 139
 120
 199
 167
259 GSQGAGRGGEGAGAAAAAAAGGAGQGGYGGLGGQGAGQGGYGGLGSQGAGRGGLGGQGAG- 317
 22
 ADDRESSEE:
 GLGSQGAGRGGLGGQGAGAAAAAAAAGGAGQGGLGGQGAGQGAGASAAAAAGGAGQGGYGGL
 AAAAAAGGAGQGGYGGLGSQGAGGGGGGGGGAGAAAAAAAG------GAGQGGYG 166
 301 No. 5989894th Washington Street
 Lewis, Randolph V.
Xu, Ming
 Length 718;
 Indels 188;
 Gaps
 185
 15;
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RESULTS CONTRIBUTION OF THE CONTRIBUTION OF TH	
SEGULT 4 5-08-209-747-2 5-08-209-747-2 Patent No. 573371 GENERAL INFORMATION: APPLICANT: Lewis, Randolph V. APPLICANT: Lewis, Randolph V. APPLICANT: CLOyin, Mark TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider TITLE OF INVENTION: Silk Proteins NUMBER OF SEQUENCES: 56 CORRESPONDENCE ADDRESS: STREET: P.O. BOX 747 CITY: Falls Church STATE: Virginia COUNTR: Galls Church STATE: Virginia COUNTR: USA ZIP: 22040-3487 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: PATENTION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTION SYSTEM: PC-DOS/MS-DOS SOFTWARE: MIPPHY JIF., Gerald M. REDISTRATION NUMBER: US,707 REPLECATION STEER: PATENTION: NAME: MIPPHY JIF., Gerald M. REDISTRATION INFORMATION: PELECOMMUTICATION INFORMATION: PELECOMMUTICATION INFORMATION: PELECOMMUTICATION INFORMATION: SEQUENCE CHARACTERISTICS: LENGTH: 832 amino acids STRANEDENESS: 31091e TOPOLOGY: linear MOLECULE TYPE: protein MYPOTHETICAL: NO RRANISM: N. clavipes	233 AAAAGGAGQGGLGGQGAGAAAAAGGAGQGGYGGLGSQGAGRGGQGAGA-AAA 284

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; NAME/KEY:
; LOCATION:
US-08-209-747-2
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 US-08-458-298-2
 Query Match 49.8%; Score 1343.5; I Best Local Similarity 47.9%; Pred. No. 1e-91; Matches 343; Conservative 19; Mismatches 1
 Sequence 2, Application US/08458298 Patent No. 5756677
 GENERAL INFORMATION:
APPLICANT: Clevis, Randolph V.
APPLICANT: Clyin, Mark
APPLICANT: Clyin, Mark
TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider
TITLE OF INVENTION: 51k Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
 TISSUE TYPE: FEATURE:
 390
 193
 569
 449 YGAGAGAAAAAATGAGGAGGYGRGAGAGAAAGAGAGTGGAGYGGQGGYGAGAGAGA
 270
 282
 93
 49
 93
ADDRESSEE: BI
 ----GRGAGAGGYGGQGGYGAGAGAGAAAAAAGAGAGGYGDKEIACWSRCRYTVASTTSRL
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 1..309
 Birch, Stewart, Kolasch & Birch
 minor
 ampullate gland
 DB 1;
 143;
 Indels 211;
 Length 832;
 Gaps
 508
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 US-08-458-298-2
 Query Match
Best Local Similarity
Matches 343; Conserv
 APPLICATION NUMBER: US/08/458,298
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,747
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MULTPHY JI., Gerald M.
REGISTRATION NUMBER: 28,977
REGISTRATION NUMBER: 28,977
 TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 2:
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: N. clavipes
TISSUE TYPE: minor ampullate gland
 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
 SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
 COMPUTER READABLE FORM:
 FEATURE:
 MOLECULE TYPE:
 170
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 NAME/KEY:
LOCATION:
 LENGTH: 832 amino TYPE: amino acid STRANDEDNESS: sir
 REFERENCE/DOCKET NUMBER: 14
 93
 49
 93
 TOPOLOGY:
 TELEPHONE:
 MEDIUM TYPE:
 COUNTRY: USA
 N
 GAGQGGYGGLGGQGAGQGGYGGLGSQGAGRAGGLGGQGAGAAAAAAG---GAGQGGLGGQ-- 247
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Virginia
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 Conservative
 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 linear
 Floppy disk
 protein
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 49.8%; Score 1343.5; DB 1;
47.9%; Pred. No. 1e-91;
tive 19; Mismatches 143;
 1447-104P
 DB 1;
 Indels 211;
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Length 832;

Gaps

25;

149

48

92

169

192

508

136

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-425-069-4
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 US-08-425-069-4
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 RESULT
 Query Match
Best Local Similarity 51.1
Conservative
 Sequence 4, Application US/08425069 Patent No. 5728810
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION NUMBER: US/08/425,069
FILING DATE: 19-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-106P
TELEPHONE: (703) 205-8050
TELEPHONE: (703) 205-8050
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 4:
 APPLICANT:
 CORRESPONDENCE ADDRESS:
Blich, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
STATE: Virginia
 SEQUENCE CHARACTERISTICS
LENGTH: 595 amino aci
 APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
 466
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 TYPE:
 ZIP: 22046
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 amino acid
 595 amino acids
 Xu, Ming
 Randolph V.
 42.4%; Score 1144; DB 1; 51.1%; Pred. No. 3.4e-77; tive 25; Mismatches 139
 Version #1.
 139;
 Length 595;
 Indels 136;
 Gaps
 682
 417
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 US-08-317-844B-4
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 Sequence 4,
Patent No.
 GENERAL INFORMATION:
 APPLICANT: Himman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRO NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5989894th Washington Street CITY: Falls Church
APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY Jr., Gerald M
REGISTRATION NUMBER: 28,977
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
 APPLICANT:
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 460
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 343
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 4, Application US/08317844B
5. 5989894
 22046
 Lewis, Ra
Xu, Ming
 Randolph V.
 Version
 AND A TRANSFORMED CELL AND PRODUCTS THEREOF
 459
 342
 171
 122
 519
 402
 103
 447
 358
 315
 285
 261
 210
 231
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TOPOLOGY: linear; MOLECULE TYPE: protein US-08-317-844B-4
 US-07-609-716-31
 REFERENCE/DOCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENCTH: 595 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
 Best Local Similarity Matches 313; Conserv
 Query Match
Best Local
 Sequence 31, Application Patent No. 5514581
 GENERAL INFORMATION:
 APPLICANT: Ferrari, Franco A. APPLICANT: Cappello, Joseph TITLE OF INVENTION: Functiona TITLE OF INVENTION: Synthetic
 NUMBER OF SEQUENCES:
 576
 508 PGLSGCDVLIQAL 520
 343 GPGGYGPGSASAAAAAAGPGQQGPGGYGPGQQGPSGPGSASAAAAAAAAAGPGGYGPGQQG
 316 GLGGQGAGAAAAAAAAGGAGQGGLGGQGAG-----AAAAAAAG----GAGQGG
 232 GY-----GPGQQGLSGPGSAAAAAAAAAGPGQQGPGGYGPGQQGPSGPGSAAAAAAAAAAGP
 211 GYGGLGSQGAGRGGLGGQGAGAAAAAGGAGQGGLGGQGAG-----AAAAAAAGGAGQ
 123 SGQQGPGGYGPGQ------QGPGGYGPGQQGPGGYGPGQQGPSGPGSAAAAAAAA 171
 17 GYG----GLGGQGAGQ----GAG-AAAAAAAGGAGQGGYG------GLGSQGAGR--
 ω
 PGQQGPSGPGSAAAAAAGSGQQGPGGYGPRQQGPGGYGQQQGPSGPGSAAAASAE 122
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 GYGPGQQGPGGYGPGQQGPSGPGSAAAAAAAAAAAGPGGYGPGQQGPGGYGPGQQGPGRYG 62
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 -GQGGLGGQGAGQGAGAAAAAAGGAGQGGYG----GLGSQGAGRGGSGGQG-AGAAAAAA 157
 AAASAGPGGYGPAQQGPSGPGTAASAASAGPGGYGPAQQGPAGYGPGSAVAASAGAGSAG
 PGGYAPGQQGPSGPGSASAAAAAAAAG--PGGYGP-GQQGPGGYAPGQQGPSGPGSAAAA
 LGGQGAGQ----GAGAAAAAAAAAAGGVRQGGYGGLGSQGAG-----RGGQGAG-AAAA
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 Conservative
 42.48; Score 1144; DB 2;
51.18; Pred. No. 3.4e-77;
), Joseph
Functional Recombinantly Prepared
Synthetic Protein Polymer
118
 US/07609716
 25;
 1447-105P
 Mismatches 139;
 Length 595;
 Indels 136;
 Gaps
 210
 575
 519
 447
 459
 407
 402
 358
 342
 315
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 231
 30;
 ; TOPOLOGY: 11; MOLECULE TYPE: US-07-609-716-31
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 Query Match
Best Local S
 Matches
 INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS: LENGTH: 1177 amino acids
 NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55186-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 ATTORNEY/AGENT INFORMATION: NAME: Rowland, Bertram I
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palantin
 993
 933
 813
 693
 345
 753
 633 GAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
 CITY:
STATE:
 LENGTH: 1177 amin
TYPE: amino acid
STRANDEDNESS: si
 TELEPHONE: 415 / TELEPHONE: 415-398-3249
 17 GYGGLGGQGAGQGAGAAAAAAAG-----GAGQGGYGGLGSQGAGRG-GQGAGAAAAAAAGG
 Local Similarity
nes 243; Conserv
 FILING DATE: 0 CLASSIFICATION:
 APPLICATION NUMBER: US/07/609,716 FILING DATE: 06-NOV-1990
 STREET:
 ADDRESSEE:
 AGQGGYGGLGS-QGAGRGGLGGQGAGAAAAAAGGYGQGGLGGQGAGQGAGAAAAAAAGGAGQ
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 AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGA 752
 GAGAGSGAGAGSGAGAGSGAAGSGAAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
 94111
 San Francisco
CA
 E: Flehr, Hohbach, Test, Albritton & Herbert Four Embarcadero Center, Suite 3400
 Conservative
 PatentIn Release #1.0, Version
 linear
 protein
 single
 36.0%; Score 972; DB 1 44.1%; Pred. No. 3e-64;
 -AGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGAGAMDPG-----
 30;
 Mismatches
 DB 1; Length 1177;
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224; Indels

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 US-08-175-155-29
 Query Match 36.0%; Score 972; DB 1; Length 117; Best Local Similarity 44.1%; Pred. No. 3e-64; Matches 243; Conservative 30; Mismatches 224; Indels
 Sequence 29,
 GENERAL INFORMATION:
 TELEPHONE: 415-781-1989
TELEPAX: 415-398-3249
TELEPAX: 415-398-3249
TREORMATION FOR SEG ID NO: 29
SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
 tent No. 5641648
 APPLICANT: C
APPLICANT: C
APPLICANT: C
APPLICANT: I
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,155
FILING DATE: 29-DEC-1993
CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETTAM II.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
 TITLE OF INVENTION: Methods for Preparing Synthetic TITLE OF INVENTION: Repetitive DNA NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS
 693
873 GSGAGAGSGAGAGSGAGAGSGAAGSGAAGSGAGAGSGAGAGSGAGAGSGAGAG 932
 185
 753
 633 GAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSG 692
 71
 17 GYGGLGGOGAGAAAAAAAAG-----GAGQGGYGGLGSQGAGRG-GQGAGAAAAAAAGG 70
 COUNTRY: US
ZIP: 94111
 TYPE: amino acid
 STREET:
 ADDRESSEE:
 AAAAAAAG---GAGQGGYGGLG-GQGAGQGGYG-GLGS-QGAGRGGLGGQGAGAAAAAG- 237
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 SSEE: Flehr, Hohbach, Test, Albritton & Herbert T: Four Embarcadero Center, Suite 3400 San Francisco
 S
 Application US/08175155
 Crissman, John W.
 Ferrari, Franco A.
 A-55186-5/BIR
 DB 1; Length 1177;
 54;
 Gaps
 872
 812
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 RESULT 10
US-08-477-509B-64
 Sequence 6 Patent No.
 GENERAL INFORMATION:
 INFORMATION FOR SEQ
 PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-CCT-1987
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino aci
 CURRENT APPLICATION DATA:
 APPLICANT: Dorman, Mary A
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
NUMBER OF SEQUENCES: 112
 1160 RYQLSAGRYHY 1170
 TELEPHONE: 415-781-1989
 FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 PRIOR APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 APPLICANT:
 APPLICANT:
 1113 GAGSGAG-----AGSGAGAGSGAGSGAGAGSGAGAGSGAGAMDPG-----
 1053 AGAGSGAGAGSGAGAGSGAAGSGAAGSGAGAGSGAGAGSGAGAGSGAGAGSGA 1112
 516 LIQALLGHHHH
 399 ---GQGAGAAAAAAGGAGQGGTGGLGGQGVGAGGLGGQGAGAAAAVGAGQGGYGGVGSGA 455
 993 GAGAGSGAGAGSGAGAGSGAAGSGAAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
 933 SCAGAGSGAGAGSGAGAGSGAGAGSGAAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 992
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
 APPLICATION. NUMBER: US/08/477,509B FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
 REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
 APPLICATION NUMBER: US 08/175,155 FILING DATE: 29-DEC-1993
 COUNTRY:
 CITY: San Francisco
STATE: California
 STREET:
 TELEPHONE:
 ADDRESSEE:
 SAASAAASRLSSPQASSRVSSAVSNLVASGPTNSAALSSTISNVVSQIGASNPGLSGCDV 515
 GAAAAAAAGGAGQGGLGGQGAGQGAGAA-----AAAAAAAAAGGVRQGGYGGLGS-QGAGRG 398
 AAGGAGQGGYGGQGAGQGGYGGLGSQGAGRGGLGGQGAGAAAAAAAAAGGAGQGGLGGQGA
 64,
 94111
 *, Application US/08477509B
5770697
 Trecartin, Richard F.
 E: Flehr, Hohbach, Test, Albritton & Herbert Four Embarcadero Center, Suite 3400
 415-398-3249
 Crissman, John w
 .177 amino acids
 PatentIn Release #1.0, Version #1.30
 Ferrari, Franco A
 Floppy disk
 UMBER: US 06/927,258
04-NOV-1986
 526
 ID NO:
 64:
 1052
 344
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STRANDEDNESS: single;
; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-477-509B-64
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 US-08-707-237A-35
 Query Match 36.0%; Score 972; DB 1; I Best Local Similarity 44.1%; Pred. No. 3e-64; Matches 243; Conservative 30; Mismatches 224;
 Patent No. 5830713
GENERAL INFORMATION:
 Sequence 35, Application US/08707237A Patent No. 5830713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 APPLICANT: DOIMAN, MATY A.
TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
TITLE OF INVENTION: REPETITIVE DNA
 APPLICANT: Ferrari, Franco A. APPLICANT: Capello, Joseph APPLICANT: Crissman, John W.
 1160 RYQLSAGRYHY 1170
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 693
 516 LIOALLGHHHH
 813 AGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGA
 CITY: San Francisco
STATE: California
 17 GYGGLGGQGAGAGAAAAAAG-----GAGQGGYGGLGSQGAGRG-GQGAGAAAAAAGG
 COUNTRY: United States ZIP: 94111-4187
 71 AGQGGYGGLGS-QGAGRGGLGGQGAGAAAAAGGVGQGGLGGQGAGAGAGAAAAAAGGAGQ 129
 STREET:
 ADDRESSEE:
 AAAAAAAG---GAGQGGYGGLG-GQGAGQGGYG-GLGS-QGAGRGGLGGQGAGAAAAAG-
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 SGAGAGSGAGAGSGAGAGSGAAGSGAAGSGAGAGSGAGAGSGAGAGSGAGAGS
 E: Flehr, Hohbach, Test,
Four Embarcadero Center,
 ····AGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAMDPG·····
 108
 Albritton
Suite 3400
 DB 1; Length 1177;
 & Herbert
 Indels
 54;
 Gaps
 932
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 398
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 US-08-707-237A-35
 Matches
 Query Match
 TELEFAX: (415) 398-324:
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 APPLICATION NUMBER: US 06/927
FILING DATE: 04-NOV-1986
ATTORNEY_AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTATION NUMBER: 31.8-01
REFERENCE/DOCKET NUMBER: A-51
TELECOMMUNICATION INFORMATION:
 STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
 FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 09-NOV-1988
 FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609,716
 SOFTWARE: PatentIn Release #1.0, VeCURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/707,237A
FILING DATE: 03-SEP-1996
 APPLICATION NUMBER: US 0 FILING DATE: 29-OCT-1987 PRIOR APPLICATION DATA:
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 FILING DATE: 09-NOV-PRIOR APPLICATION DATA:
 FILING DATE: 29-DEC-
PRIOR APPLICATION DATA:
 345
 633 GAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSG
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 Local Similarity
nes 243; Conserv
 TYPE:
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 TELEPHONE:
 APPLICATION NUMBER:
 APPLICATION NUMBER:
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 (415) 399
 1177 amino acids
 Conservative
 PatentIn Release #1.0, Version #1.30
 UMBER: US 08/175,155
29-DEC-1993
 398-3249
 781-1989
 36.0%; Score 972; DB 2; Length 1177; 44.1%; Pred. No. 3e-64;
 PC-DOS/MS-DOS
 US 06/927,258
 US 07/269,429
 US 07/114,618
 US 08/053,049
 30;
 A-55186-10/WHD
 Mismatches
 224; Indels 54;
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1052

344 932 284

992

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 US-08-482-085B-64; Sequence 64, Ap
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US-08-482-085B-64
 RESULT 12
 Patent No. 6018030
GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: UI
FILING DATE: 22 APR-11
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UI
 APPLICATION NUMBER: US 01
FILING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 29-OCT-1987
 SOFTWARE: PATENCLI NATA:
CURRENT APPLICATION DATA:
US/08/482,085B
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
 APPLICANT:
APPLICANT:
 RECISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 1113 GAGSGAG-----AGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAMDPG----- 1159
 1053 AGAGSGAGAGSGAGAGSGAGAGSGAAGSGAGAGSGAGAGSGAGAGSGAGAGSGA 1112
 TOPOLOGY: 1
MOLECULE TYPE:
 SEQUENCE CHARACTERISTICS
 ATTORNEY/AGENT INFORMATION:
 1160 RYQLSAGRYHY 1170
 APPLICANT:
 APPLICANT:
 APPLICANT:
 456
 APPLICANT:
 516 LIQALLGHHHH 526
 399
 APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
 STREET:
 STRANDEDNESS:
 TYPE: amino acid
 TELEPHONE:
 NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,803
 FILING DATE:
 COUNTRY:
 CITY: San Francisco
 ADDRESSEE:
 ---GQGAGAAAAAAGGAGQGGTGGLGGQGVGAGGLGGQGAGAAAAVGAGQGGYGGVGSGA 455
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 9411
 California
 Application US/08482085B
 E: Flehr, Hohbach, Test, Albritton & Herbert Four Embarcadero Center, Suite 3400
 415-398-3249
 Cappello, Joseph
Crissman, John W.
 S
 Causey, Stuart
Pollock, Thomas J.
 Richardson,
 PatentIn Release #1.0, Version #1.30
 Chambers, James
 linear
 amino acids
 peptide
 29-DEC-1993
 22-APR-1993
 single
 Franco A.
 us 06/927,258
 US 08/053,049
 US 08/175,155
 US 07/114,618
 Charles
 A-55186-6/RFT/MTK
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 US-08-475-411A-31
 Sequence 31, Application US/08475411A Patent No. 6140072
 Query Match
Best Local Similarity
 GENERAL INFORMATION:
 ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
 NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
 APPLICANT: Cappello, TITLE OF INVENTION: I
 APPLICANT:
 1160 RYQLSAGRYHY 1170
 1053 AGAGSGAGAGSGAGAGSGAAGSGAAGSGAGAGSGAGAGSGAGAGSGAGAGSGA 1112
PRIOR APPLICATION DATA
 130 GGYGGLGS---QGAGRGGSGGQGAGAAAAAAG-GAGQGGYGGLGS-QGAGRGGLGGQGAG
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 456 SAASAAASRLSSPQASSRVSSAVSNLVASGPTNSAALSSTISNVVSQIGASNPGLSGCDV 515
 933 SGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS
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 633 GAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSG
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 238 ----GAGQGGLGGQGAGAAAAAAGGAGQGGYGGLGSQGAGRG------GQGAGAAAA 284
 ADDRESSEE: Flehr, HO STREET: Four Embarco CITY: San Francisco
 71 AGQGGYGGLGS-QGAGRGGLGGQGAGAAAAAGGYGQGGLGGQGAGGAGAAAAAAGGAGQ 129
 17 GYGGLGGQGAGQGAGAAAAAAAGG-----GAGQGGYGGLGSQGAGGG-GQGAGAAAAAAAGG
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 APPLICATION NUMBER:
 COUNTRY:
 STATE:
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 243;
 CA
 SD
 Conservative
 Ferrari, Franco A.
 Floppy disk
 07-JUN-1995
 36.0%;
44.1%;
 Functional Recombinantly Prepared Synthetic Protein Polymer 119
 Joseph
 US/08/475,411A
 30;
 Score 972; DB 3; I
Pred. No. 3e-64;
30; Mismatches 224;
 Version
 Length 1177;
 54;
 Gaps
 455
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 17;
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US-08-475-411A-31
 Query Match
 TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
 FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
 TOPOLOGY: 11 MOLECULE TYPE:
 SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino aci
 REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
 1113 GAGSGAG-----AGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAMDPG-----
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 993
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 633 GAGAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSG
 693 AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAAGSGAGAGSGAGAGSGAGAGSGAGAGSGA 752
 71
 17 GYGGLGGQGAGQAAAAAAAAG-----GAGQGGYGGLGSQGAGRG-GQGAGAAAAAAAGG
 Local Similarity
les 243; Conserv
 STRANDEDNESS:
 TYPE: amino acid
 APPLICATION NUMBER:
 APPLICATION NUMBER: US 07/269,429 FILING DATE: 09-NOV-1988
 ---GQGAGAAAAAAGGAGQGGTGGLGGQGVGAGGLGGQGAGAAAAVGAGQGGYGGVGSGA 455
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 LIQALLGHHHH 526
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 SGAGAGSGAGAGSGAGAGSGAAGSGAAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS
 AAGGAGQGGYGGQGAGYGGLGSQGAGRCGLGGQGAGAAAAAAAAAGGAGQGGLGGQGA 344
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 AGQGGYGGLGS-QGAGRGGLGGQGAGAAAAAGGYGQGGLGGQGAGQGAGAAAAAAAGGAGQ 129
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 1177 amino acids
 415-398-3249
 36.0%; Score 972; DB 4 ilarity 44.1%; Pred. No. 3e-64; Conservative 30; Mismatches 2
 linear
 protein
 single
 US 06/927,258
 DB 4; Length 1177;
 224; Indels 54; Gaps
 1052
 1112
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 Sequence 31, Application US/08478029A Patent No. 6184348
 Matches
 Query Match 36.0%; Score 972; DB 4
Best Local Similarity 44.1%; Pred. No. 3e-64;
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO:
 APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
 APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
 FILING DATE: 29-OCT-PRIOR APPLICATION NUMBER:
 SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 FILING DATE: 04-NOV-1986 ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
 MOLECULE TYPE: protein
 SEQUENCE CHARACTERISTICS:
185 AAAAAAAG---GAGQGGYGGLG-GQGAGQGGYG-GLGS-QGAGRGGLGGQGAGAAAAAG-
 633 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
 APPLICATION NUMBER: US 0 FILING DATE: 06-NOV-1990
 COUNTRY: U
ZIP: 94111
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
 17 GYGGLGGQGAGAAAAAAAAG-----GAGQGGYGGLGSQGAGRG-GQGAGAAAAAAAGG
 TYPE: amino acid
STRANDEDNESS: si
 REGISTRATION NUMBER:
 APPLICATION NUMBER: US/08/478,029A FILING DATE: 07-JUN-1995
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 TOPOLOGY:
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 GAGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAG
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 AGQGGYGGLGS-QGAGRGGLGGQGAGAAAAAAGGYGQGGLGGQGAGGAGAAAAAAAGGAGQ 129
 San Francisco
 CA
 Trecartin, Richard F
 1177 amino acids
 SD
 415-398-3249
 Conservative
 linear
 single
 US 06/927,258
 US 07/609,716
 31,801
 30;
 A-55186-8/RFT/MTK
 Mismatches 224; Indels 54;
 DB 4; Length 1177;
 #1.30
 Gaps
 812
 70
 237
 752
 692
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RESULT 15
US-08-175-155-48
Sequence 48, Application US/08175155
Patent No. 5641648
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 GENERAL INFORMATION:
 TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
LENGTH: 1059 amino aci
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/175,155 FILING DATE: 29-DEC-1993
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test,
STREET: Four Embarcadero Center,
 APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W.
 1160 RYQLSAGRYHY 1170
 1113
MOLECULE TYPE:
 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 TITLE OF INVENTION: Methods for Preparing Synthetic TITLE OF INVENTION: Repetitive DNA NUMBER OF SEQUENCES: 69
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 1053 AGAGSGAGAGSGAGAGSGAGAGSGAAGSGAGAGSGAGAGSGAGAGSGAGAGSGA 1112
 APPLICANT:
 516 LIQALLGHHHH 526
 399
 993
 345
 933
 873
 285 AAGGAGQGGYGGQGAGQGGYGGLGSQGAGRGGLGGQGAGAAAAAAAAAAAAGGAGQGGLGGQGA 344
 813 AGSGAGAGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGA
 NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55186-5/BIR
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TYPE: amino acid
STRANDEDNESS: si
 COUNTRY: U
 TOPOLOGY:
 GAAAAAAGGAGQGGLGGQGAGQGAGA-----AAAAAAAAGGVRQGGYGGLGS-QGAGRG
 GAGSGAG-----AGSGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAMDPG-----
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 ---GOGAGAAAAAAGGAGOGGTGGLGGOGYGAGGLGGOGAGAAAAYGAGOGGYGGYGSGA 455
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 SGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS
 ----GAGQGGLGGQGAGAAAAAAGGAGQGGYGGLGSQGAGRG------GQGAGAAAA 284
 San Francisco
 Ç
 1059 amino acids
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 Dorman, Mary A.
 peptide
 single
 Albritton & Herbert
Suite 3400
 1052
 932
 872
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Query Match

35.6%;

Score 962.5;

DB 1;

Length 1059;

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 Best Local Similarity 45.4%; Py Matches 244; Conservative 33;
1002 GSGAGAGSGAGAGSGAGAGSGAGAGSGAGAMDPG-----RYQLSAGRYHY 1052
 415 G-----GTGGLGGQGVGAGGLGGQGAGAAAAVGAGQGGYGGVGSGASAASAAASRLSSPQ 469
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 942 GSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGA 1001
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 823 SGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG
 703 SGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG
 187 AAAAAG---GAGQGGYGGLG---GQGAGQGGYGGLGS-QGAGRGGLGGQGAGAAAAAG-G
 583 SGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG
 75 GYGGLGS-QGAGRGGLGGQGAGAAAAAG----GYGQGGLGGQGAGQGAGAAAAAAAGGAGQG 130
 17 GYGGLGGQGAGQGAGAAAAAAAG-GAGQGGYGGLGSQGAGRG-GQGAGAAAAAAAGGAGQG
 Pred. No. 1.4e-63;
33; Mismatches 225;
 Indels
 35;
 Gaps
 355
 702
 882
 822
 296
 238
 642
 582
 74
 18;
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Search completed: July 3, 2001, 14:56:45 Job time: 535 sec

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Minimum DB
Maximum DB
 Perfect score:
Sequence:
 Title:
 OM protein -
 Database
 Post-processing: Minimum Match 0%
Maximum Match 10
 Total number of hits satisfying chosen parameters:
 Scoring table:
 9
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
1148
968.5
93.5
912.7
912.7
912.8
8866.5
866.5
866.5
858.8
859.5
847
844
843.8
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 Score
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 length: 0
length: 2000000000
 Query
Match
 BLOSUM62
Gapop 10.0 ,
 July 3, 2001, 14:59:40; Search time 63.58 Seconds (without alignments) 632.591 Million cell updates/sec
 US-09-490-291-8
2700
 PIR_68:*
 219241 segs, 76174552 residues
 Listing
 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
 MASMTGGQQMGRIRIRGYGG......GLSGCDVLTQALLGHHHHHH
 pir1:*
pir2:*
pir3:*
pir4:*
 Length DB
Match 100%
first 45 summaries
 Gapext 0
 A36068
A44112
T31328
 SUMMARIES
 219241
 hypothetical glyci
hypothetical glyci
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697.5	714.5	729.5	732	736	739.5	742.5	747	747.5	748.5	764.5	781.5	782.5	783.5	793	796.5
25.8	26.5	27.0	27.1	27.3	27.4	27.5	27.7	27.7	27.7	28.3	28.9	29.0	29.0	29.4	29.5
481	338	860	594	384	591	639	615	618	584	606	694	603	408	576	837
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A35628	KNMU	EAMS	G70545	A26099	в70523	D70931	н70589	A70989	G70804	H70816	.F70868	A70770	S57483	A70900	E70835
loricrin - mouse	glycine-rich cell	elastin precursor	hypothetical glyci	glycine-rich cell	hypothetical glyci	glycin-rich protei	hypothetical glyci	hypothetical glyci							

## ALIGNMENTS

A; Molecule type: DNA A; Residues: 1-718 < XNA A; Cross-references: GB:M37137; NID:g159711; PID:g159712 A; Note: the authors translated the codon GGT for residue R;Xu, M.; Lewis, R.V.
Proc. Natl. Acad. Sci. U.S.A. 87, 7120-7124, 1990
A;Title: Structure of a protein superfiber: spider
A;Reference number: A36068; MUID:90384959
A;Accession: A36068 major ampullate fibroin protein - orb spider (Nephila clavipes) (fragment)
C;Species: Nephila clavipes
C;Date: 08-Mar-1991 #sequence_revision 13-Jan-1993 #text_change 09-Sep-1997
C;Accession: A36068 A; Status: preliminary Query Match
Best Local Similarity
Matches 477; Conserv 233 AAAAGGAGQGGLG----GQGAGAAAAAAAGGAGQGGYGGLGSQGAGR----GGQGAGA-AAA 259 GSQGAGRGGEGAGAAAAAAGGAGQGGYGGLGGQGAGQGGYGGLGSQGAGRGGLGGQGAG-167 GLGSQGAGRGGLGGQGAGA-----6 GGQQMGRIRIRGYGGLGGQGAGQGAGAAAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAAA AA-----AAGGAGQGGYGGLGSQGAGRGGQGAGAAAAAAGGAGQRGYGGLGNQGAGRGGLGGQGAGA AAGGAGQGGYGG----QGAGQG-----**AAAAGGAGQGGLGGQGAGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGLGGQGAGAVAAA** GLGSQGAGRGGLGGQGAGAAAAAAAAGGAGQGGLGGQGAGQGAGASAAAAAGGAGQGGYGGL Conservative 81.1%; -----AAAAAGGAGQ----6, Score 2190; DB 2 Pred. No. 3e-112; 6; Mismatches 1 -----GYGGLGSQGAGRGGLGGQGAGA 324 DB 2; Length 718; 10; dragline Indels 188; 292 as Gln, silk Gaps GTA for residue 198 437 166 284 317 232 65 258 185 15;

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spidroin 2, dragline silk fibroin - orb spider (Nephila clavipes) (fragment)
N;Alternate names: silk fibroin, dragline
C;Species: Nephila clavipes
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Mar-1998
C;Accession: A44112; S27824
R;Hinman, M.B.; IteVis, R.V.
J. Biol. Chem. 267, 19320-19324, 1992
A;Title: Isolation of a clone encoding a second dragline silk fibroin. Nephila clavipes
A;Reference number: A44112; MUID:92406876
A;Accession: A44112
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
 A;Molecule type: mRNA
A;Residues: 1-627 <HINA
A;Cross-references: GB:M92913; NID:g159713; PID:g159714
A;Cross-references: GB:M92913; NID:g159713; NID:g159713;
 A; Molecule type: mRNA
A; Residues: 19-627 <HI2>
A; Cross-references: EMBL: M92913
 A; Reference number: S27824
A; Accession: S27824
 Query Match
Best Local S
Matches 314
286
 172
 158
 123
 674
 486
 614
 426
 558
 366
 498
 104
 63
 17
 57
 7 Match 42.5%; Score 1148; DB 2; Local Similarity 51.1%; Pred. No. 8.6e-56; Nes 314; Conservative 25; Mismatches 139
 w
 PTNSAALSSTISNVVSQIGAS 506
 GGYG----GLGSQGAG-RGGQGAG-AAAAAAGGAGQGGYGGQGGYGGLGSQGAGRG 315
 GAGGLGGQGAGAAAAVGAGQGGYGGVGSGASAASAASRLSSPQASSRVSSAVSNLVASG 485
 GYGGLGSQGAGRGGLGGQGAGAAAAAGGAGQGGLGGQGAG-----AAAAAAAGGAGQ
 GGAGQ---GGYG----GLGSQGAGRGGLGGQGAGAAAAAAAGGAGQGGYGGLGGQGAGQG
 -GQGGLGGQGAGAAAAAAAGGAGQGGYG----GLGSQGAGRGGSGGQG-AGAAAAAA 157
 GYG----GLGGQGAGQ----GAG-AAAAAAAGGAGQGGYG------GLGSQGAGR-- 56
 GRGGLGGQGAGAAAAGGAGQGGYGGVGSGASAASAASRLSSPQASSRLSSAVSNLVATG
GGYGPGQQGPGGYGPGQQGPSGAGSAAAAAAAGPGQQGLGGYGPGQQGPGG---YGPGQQ
 GY-----GPGQQGLSGPGSAAAAAAAAGPGQQGPGGYGPGQQGPSGPGSAAAAAAAAAAA
 SGPGQQGPGGYGPGQQGPGGYGPGQQGPSGPGSAAAAAAAAASGPGQQGPGGYGPGQQGPG
 SGQQGPGGYGPGQ------QGPGGYGPGQQGPGGYGPGQQGPSGPGSAAAAAAAA
 PGQQGPSGPGSAAAAAAAGSGQQGPGGYGPRQQGPGGYGQGQQGPSGPGSAAAASAASAA 122
 AAAVGAGQEGIRGQGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAAGGAGQGGLGGQGAG
 ----GGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGLG-GQ----GAGAAAAAGGV----
 AAAAAAGGAGQGGYGGLGNQGAGRGGQGAAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAAA 497
 25; Mismatches 139;
 ---GGLGGQGAGAAAAAAGGAGQGGLGGQGAG
 Length 627;
 Indels 136;
 Gaps
 365
 171
 62
 673
 557
342
 285
 231
 210
 30;
 R;Sezutsu, H.; Tamura, T.; Yukuhiro, K.
submitted to the EMBL Data Library, August 1998
submitted to the EMBL Data Library, August 1998
spescription: Characterization of the full length fibroin
 fibroin - Chinese oak silkmoth
C;Speckes: Antheraea pernyi (Chinese oak silkmoth)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T31328
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 A; Molecule type: DNA
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A; Introns: 14/3
 A; Status: preliminary; translated from GB/EMBL/DDB:
 A;Cross-references: EMBL:AF083334; NID:g3450882; PID:g3450883; PIDN:AAC32606.1
 Query Match
Best Local Similarity
 Matches
 1140
 1080
 1020
 201
 184
 150
 960
 128
 900
 840
 780
 508 PGLSGCDVLIQALL 521
 520
 448
 460
 408
 403
 359
 343
 316
 576 PGLSGCDVLIQALL 589
 67
 17 GYG-GLGGQGAGQAAAAAAAAAGGAGQGGYGGLGSQGAGRGGQG-----AGAAAA 66
 AAASGAGGSGGGYGWGDGGYGSDSAAAAAAAAAAAAAAASGAGGSGGYGGYGSDSAAAAAA 1199
 ----GLGGQGAGQG-GYGGLGSQGA-----
 GAAAAAA-----AGGAGQGGYG-----
 AAAAAAASGARGSGGYGGYGSDSAAAAAAAAAAAAAAAGSGAGGVGGGYGWGDGGYGSDSAA 1079
 AGGSGGGYGWGDGGYGSDSAAAAAAAAAAAAAAAAGSGAGGGYGWGDGGYGSDSAAAAAA 1019
 AAAGGVGQGGLGGQGAGQGAGAAAAAAGGA-----
 GYGWGDGGYGSDSAAAAAAAAAAAAAGSGAGGGGYGWGDGGYGSDSAAAAAAAAAAAAA 839
 LGGQGAGQ----GAGAAAAAAAAAAGGVRQGGYGGLGSQGAG------RGGQGAG-AAAA 407
 GPGGYGPGSASAAAAAAAGPGQQGPGGYGPGQQGPSGPGSASAAAAAAAAAAAGPGGYGPGQQG
 GLGGQGAGAAAAAAAAGGAGQGGLGGQGAG-----
 AAAAAAAAAAAGSGAGGRGDGGYGSGSSAAAAAAAAAAAARRAGHDRAAGSAAAAAAAAAA 1139
 AGAAAAAGGAGQGGYGGLGSQ----
 -----GQGGYG------GLGSQGAGRG---GSGGQG-----
 ASGARGSGGYGGYGSDSAAAAAAAAAAAAAAGSGAGGYGGGYGWGDGGYGSDSAAAAAAAAA 899
 AAAAAGPGGYGPAQQGPSGPGIAASAASAGPGGYGPAQQGPAGYGPGSAVAASAGAGSAG
 AAAAGSGAGGRGDGGYGSGSSAAAAAAAAAAAASAARRAGHDSAAGSAAAAAAAAAAAAAAASG
 AAGGAGQGGTG----GLGGQGV-----GAGGLG-----GQGAGAAAAVGAGQGG
 287;
 Conservative
 35.9%; Score 968.5; DB 2; 34.7%; Pred. No. 1.5e-45; tive 30; Mismatches 160;
 -GRGGLGGQG-----A 230
 Indels
 Length
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A;Experimental source: strain H37Rv C;Genetics:
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: F70806
 hypothetical glycine-rich protein Rv3508 - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: F70806
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 A: Molecule type: DNA
A: Residues: 1-1901 <COL>
A: Cross-references: GB: AL022022;
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 A; Gene: Rv3508
C; Superfamily:
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H
 1320
 1260
 448
 663
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 59
 Local Similarity
 ر.
 GGTNGSGGAGGAGGKGGTGGAGGSGADNPTGAGFAGGAGGTG-GAAGAGGAGGATGTGGT
 TGGO--QMGRIRIRGYGGLGGQGAGQGAGAAAAA----AAGGAG-QGGYGGLGSQGAGRGG 58
 RGDGGYGSGSSAAAAAAAAAAAARRAGHDRAAGSAAAAAAAAAAAAAA 1607
 Y--GGVGSGASAASAASRLSSPQASSRVSSAVSNLVASGPTNSAALS
 GSGSSAAAAAAAAAAAAARRAGHDRAAGSAAAAAAAAAAAAAAAGGAGGSGGGYGWGDGGYG
 SAAAAAAAAAAAAAAAAAGSGAGGAGGGYGWGDGGYGSDSAAAAAAAAAAAAAAAGSGAGGRGDGGY 1319
 GAGQGAGAAAAAAGGAGQGGYGGLGSQGAG-----RGGSGGQGAGAAAAAAGG-----
 QGAGAAAAAAGGAGQGGYGGLGSQGAGR------GGLGGQGAGAAAAAGGVGQGGLGGQ 111
 TGGAVGSVGNAGIGGTGGTGGVGGAGAGAAAAAGSSATGGAGFAGGAGGEGGAGGNSGV 722
 GGYGSDSAAAAAAAAAAAAAGSGAGGAGGGYGWGDGGYGSYSAAAAAAAAAAAAAAGSGAGG
 QG-----AGAAAAAAAAAAGGVRQGGYGGLGSQGAGGAGAAAAAAGGAGQGGT 417
 AAAAAAAGSGAGGAGGGYGWGDGGYGSDSAAAAAAAAAAAAASGAGGSGGYGGYGGYGSD
 GAAAAAAGGAGQGGLGG-------QGAGAAAAAAAAGGAGQGGYGGLGSQGAG
AGGNGGDGGDGATGAAGLGDNGGVGGDGGAGGAAGNGGNAGVGLTAKAGDGGAAGNGGNG
 GGVVGATGSAGIGGAGGRGGDGGDGASGLGLGLSGFDGGQGGQGGAGGSAGAGGINGAGG
 -AGQGGYGGLGSQGAG----RGGLGGQ-GAGAAA-----
 RGGQGAGAAAAAAGGAGQGGY------
 collagen alpha 1(IV) chain
 -AAAAAAAAGGAGQGGLGGQG------AGAAAAAAAGGAGQGGL-GCQGAG
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 34.6%;
 Pred. No. 7.6e-44;
 Mismatches
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 ----GLGSQGAGRG--
 Length 1901;
 ·GLGGQGAG-----
 ---- AAAAGGAGQG
 493
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 AASRLSSPQASSRVSSAVSNLVASGPTNSAALSSTISNVVSQIGASNPGLSGCD
 NAGVGLTAKAGDGGAAGNGGNGGAGGAGGAGGANNFNGGQGGAGGQGGQGGLGGASTTSIN
 GGPDGGDGGQGGIGGDGGNAGFGAGVPGDGGDGGNAGFGAGVPGDGGIGGTGGAGGAGGA
 VGGDGGEGASGLGLGLSGFDGGQGGQGGAGGSAGAGGINGAGGAGGTGGAGGDGAPATLI
 ANGGAGGNGGTGGKGGAGGAGTLGVGGSGGTGGDGGDAGSGGGGGGGGGAAGKAGGGGNGG
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 GYGGLGGQG-----AGQGGYGGLGSQG-----
 -AGGAGQGGLGGQG------AGQGAGAAAAAAAAAAAGGVRQGG
 -----GRGGQGAGAAAAAAGG-----AGQGGTGGLGGQGV-----
 ---AAAAAGGA-----GQGGLGGQG----AGAAAAA--
 -- AGRGGLGGQ-GAGAAAA
 514
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 1260
 1140
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 425
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gc Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987

A;Accession: B70807 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-1079 <COL> A;Cross-references: GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA17749.1; PEXPERIMENTAL SOURCE: Strain H37RV C;Genetics: hypothetical glycine-rich protein Rv3512 - Mycobacterium tuberculosis (strain H37RV) c;Species: Mycobacterium tuberculosis C;Decies: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: B70807 Ş Ъ A;Gene: Rv3512 C;Superfamily: ρy 315 48 Local Similarity 40.2 Local Similarity 40.2 -GLGSQGAGRGGQGAGAAAAAAGGAG-----QGGYGGLGSQG-----AGRGGLGGQGA AGGAAGSNGGTVGANGTGGDGGNGGAAGAATAGSNGGAGTGSAGGNGGTGGRGGSGGAGG ASMTGGQQMGRIRIRGYGGLGGQG------AGQGAGAAAAAAAAGGAGQGGYG----collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolc 34.3%; Score 927; DB 2; Length 1079; 40.2%; Pred. No. 1.3e-43; ative 14; Mismatches 202; Indels 13 Indels 138; 94 374 47 23; Holroyd, PID: 9292 geno

P 64 B

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GAAAAAGGVGQGGLGGQGAGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGSGGQ-GAGAA 153

DGIGGVGGGKGGNGADGEVGGAGGAGGSGPNTSPGGNGGQGGQGGSGGAGGAAGAGGAGG

434

GANGTAGNGGQGGAGGTG---GAGAASSATNG-GSGGAGGTGGDG-GSGGAGGTGGAGGT 489

Qy       60GAGAAAAAGGAGGGYGGLGSQGAGRGGLGGQ-GAGAAAAAGGV 103         Qy	ຜ່າວ	A; Accession: D70807 A; Accession: D70807 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-1489 <col/> A; Cross-references: GB: ALO22022; GB: AL123456; NID: g3261554; PIDN: CAA17751.1; PID: g292445 A; Experimental source: strain H37Rv C; Genetics: A; Gene	C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: D70807 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Tille: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987	GGYGGVGSGASAASAA 4 	TESEDGGAGGNGGAAGTEGTGGDGGLTGTGGTGGSGGTGGDGGNGADNTANNTAQAG GVRQGGYGGLGSQGAGGAGAAAAAAGGAGQGGTGGLGGQGV	Db 610 GSGGDGGDAGTGGNGGNRGNRSGNGTGGAGGNGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	
Qy 2 ASMTGGQOMGRIRIRGYGGLGGQGAGQAAAAAAAGGACQGGYGGLGSOGA 54	C;Superfamily: collagen alpha 1(IV) chain  Query Match Best Local Similarity 34.7%; Pred. No. 1.3e-41; Matches 258; Conservative 25; Mismatches 218; Indels 242; Gaps	A;Althors: Sqares, R; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comp A;Teference number: A70500; MUID:98295987 A;Accession: E70806 A;Status: preliminary; nucleic acid sequence not shown; translation not show A;Status: preliminary; nucleic acid sequence not shown; translation not show A;Molecule type: DNA A;Residues: 1-1381 <ccl> A;Cross-references: GB:AL02202; GB:AL123456; NID:g3261554; PIDN:CAA17744.1; A;Experimental source: strain H37Rv C;Genetics: A;Gene: Rv3507</ccl>	eti les les ssi rea	1	653 G 411 G 713 G	Db 534 GAGGAGGSSGAGGTNGSGGAGGTG-GQGGAGGAGADNPTGIGGTGGAGGAGAAAAA 370 Qy 329 AAAGGAGQGGLGGQ-GAGAAAAAGGAGGGGLGGQGAGQGAGA 370	196 -QGGYGGLGGQGAGDGGYGGLGSQGAGRGGLGGQGAGDGGYGGLGSQGAGRGGLGGQGAGDGGYGGLGSQGAGRGGLGGQG

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 AAGGAGQGGLGGQ-GAGAAAAAAGGAGQGGLGGQG-----AGQGAGA 370
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 GVGGAGGQGGD 821
 GASNPGLSGCD 514
 ;GTGGDGGTGGAAGAGGAGG------
 GQGGYGGVGSGASAASAASRLSSPQASSRVSSAVSNLVASGPTNSAALSSTISNVVS 501
 AAGTGGTGGMIGTTGNAGVGGAGGSSGAGGTNGSGGAGGTDGQGGAGGAGGAGADNPTG
 AGQGGTGGL----GCQGV------ 443
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 -AAGTGGTGGMIGTTGNA-- 810
 592
 533
 473
 275
 231
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Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. sciphering the biology of Mycobacterium tuberculosis from the complete number: A70500; MUID:98295987 : Î-1381 <COL> @erences: GB:ALO22022; GB:AL123456; NID:g3261554; PIDN:CAA17744.1; PID:g292 ||tal_source: strain_H37Rv SMTGGQQMGRIRIRGYGGLGGQGAGQGAGAAAAAAAGGAGQGGY------GGLGSQGA 54 1 glycine-rich protein Rv3507 - Mycobacterium tuberculosis (strain H37RV) Mycobacterium tuberculosis Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 GOSGGN-----GGSAGLWGNGGAGGAGGAGGNGGNGGWLFGAGGTGGTGA 201 507 ly: collagen alpha 1(IV) chain type: DNA reliminary; nucleic acid sequence not shown; translation not shown .; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon .; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. 537-544, 1998 ----GRGGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGLGGQGAGAA--AAAGGV-GQG 106 h 33.0%; Score 892; DB 2; Length 1381; Similarity 34.7%; Pred. No. 1.3e-41; 58; Conservative 25; Mismatches 218; Indels 242; Gaps E70806 32; geno

Qy Db	RIRGYGGLGGQGAGQGAGAGAAAAAAAGGAGQGGYGGLG-SQGAGRGGQ  :
	Query Match 32.6%; Score 880; DB 2; Length 767; Best Local Similarity 42.2%; Pred. No. 3.5e-41; Matches 245; Conservative 22; Mismatches 218; Indels 96; Gaps 26;
	A;Gene: Rv1087 C;Superfamily: unassigned collagens
	;Cross- ;Experi
	relimi:
	A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Tille: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987 A;Accession: E70895
- 10	R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
	es: Mycobacterium tuberculosis es: Mycobacterium tuberculosis 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 2/ sion: E70895
	RESULT 8
	Qy 492 LSSTISNVVSQIGASNPGLSG 512 ::       :     :  Db 859 FGGNTTSGASGSGGNGGNAGTAG 881
	Qy 439 AAVGAGQGGYGGVGSGASAASAAASRLSSPQASSRVSSAVSNLVASGPTNSAA 491
	Oy 396 GRGGGGAGAAAAAGGAG
	681 GANGGTGGSGGNGGDGGAGGIGGAGGNGIPGTGTEPAGGTGAKGGDGGAGGAGGAAG
	Qy         325         AAAAAAAGGAGQGGLGGQG
	Db 561 GGPGGTGGTGGNGGNGGNGGNGGNGGNAGNNSTNAPVGGEGGAGGDGGAGGAGG 620
	501 TGNGGHAGNTGDGGDGGTGGNGGNGTGGVNGADNTLNPDTPGGAGEPGGAGGAGGAA
	Qy 255 AAGGAGQGGYGGLGSOGA-GRGG
	OY 213 GGLGSQGKURGGLGGQGAGAAAAAGG-AGQGGLGGQ-GAGAAAA 254
	381 GAGGAAGARGALTSGGLAGGVGAGGTGGTGGTGGNGADAAAVVGFGANGDPGFAGGKGGN
	QY 184 GAAAAAAAGGAGQGGYGGLGGQGAGQGGY 212
_	Qy 148 QGAGAAAAAAGGAGQGGYGGLGSQGAGRGGLGGQGA 183

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otherical glycine-rich protein Rv2490c - Mycobacterium tuberculosis (strain H37RV)
secies: Mycobacterium tuberculosis
ite: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
coession: A70869
coession: A70869
coession: R,; Barosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
coession: A70869
coession: A70869
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coession: A70869
 ery Match 32.2%; Score 868.5; DB 2; st Local Similarity 41.5%; Pred. No. 2.7e-40; tches 245; Conservative 22; Mismatches 175;
 netics:
ne: Rv2490c
perfamily: collagen alpha 1(IV) chain
 lecule type: DNA
sidues: 1-1660 <COL>
oss-references: GB.AL021246; GB:AL123456; NID:g3261507; PIDN:CAA16067.1; PID:g279
perimental source: strain H37Rv
 itus: preliminary; nucleic acid sequence not shown; translation not shown
 307 LGSQG--AGRGGLGGQG-AGAAAAAAAAGGAGQGGLGGQ-GAGAAAAAAAGGAGQGGLGGQ 362
 259 AGQGGYGGLGSQG------AGRGGQGAGAAAAAAAGGA-GQGGYGGQGA---GQGGYGG
 332 TGG-GAGLGAQSVTFSSSLSGLSGGDGGAGGAGGAGGAGGTGGWLYG--GGGAAGSGGDG
 649 GKGGAGGAGETEGVTGATGATVHSGGNGGKGGNGADATVAGANGGKGGAGGNGGLVGDGG 708
 472 SRVSSAVSNLVASGPTNSAALSSTISNVVSQIGASNPGLSG 512
 568 GAAGGFGGISAATPSAGSEGAMGGAGGVGGNARLLGTGGAGGVGGGGGAGGDGGRGGVAT 627
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 508 SGGDGGAAGRGGAGNLGSAGGINAPAGNPGSGSVGIGGAGGAGGTAGLFGDGGAGGAGGA 567
 448 SGEGGFGGPGLAGGLFGNPGNGGVGGIGGDAAAGGAGGAGGNGGAGGNGGWLFGNGGAGG
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 60 GAGAAAAAGGGAGQGGYGGLGSQGAGRGGLGGQGA--GAAAAAGGVGQGGLGGQGAGQGA 117
 73 QGGYGGLGSQGA-----
 -GGQG-----VGAGGLGGQGAGAAAAVG--AGQGGYGGV-GSGASAASAAASRLSSPQAS 471
 -- PGPTNFGLNGAGGGGGVGGNGATGPWLFG
 ----GRGGLGGQGAGAAAAAGG---- 102
 Indels
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 Gaps
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 167
 507
 306
 258
 388
 213
 331
 271
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tyls.

C;Comment: Much of the sequence consists of tandemly repeated C;Comment: Much of the sequence consists of tandemly repeated C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8 C;Keywords: cell wall; structural protein; tandem repeat F;1-30/Domain: signal sequence #status predicted <SIG>F;31-465/Product: glycine-rich cell wall protein 1.8 #status pro
 glycine-rich cell wall protein 1.8 precursor - kidney bean C; Species: Phaseolus vulgaris (kidney bean) C; Species: 30-Sep-1989 #sequence_revision 19-May-1994 #text_change 16-Jul-1999 C; Accession: S01820 R; Keller, B.; Sauer, N.; Lamb, C.J. EMBO J. 7, 3625-3633, 1988 A; Title: Glycine-rich cell wall proteins in bean: gene structure and associa A; Reference number: S01820; MUID:89091109 A; Accession: S01820
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 A; Molecule type: DNA
A; Restdues: 1-465 <KEL>
A; Cross-references: EMBL: X13596; NID: 921002; PIDN: CAA31932.1;
C; Comment: This protein is enriched in the cell wall fraction
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 LTGGDGGVGGNGAKAAAAGGDGGQGGDGGNAGLFGDGGAGGDGADGTAAEA 1235
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 ---GAGGLGGQGAGAAAAVG-AGQGGYGG------VGSGASAASAAA 462
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Pred. No. 1.2e-40;
8; Mismatches 177;
 DB 1;
 Indels
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 PID:g21003 of young hypocotyls
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 A;Gene: Rv1091
C;Superfamily: unassigned collagens
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 Query Match 31.8%;
Best Local Similarity 42.8%;
Matches 232; Conservative 1
 421
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 202
 109 GGQGAGQGAGAAAAAAGGA----GQGGYGGLGSQG-----AGRGGSGGQGA----
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Gaps

26;

63

468 150

524

239

643

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A70896
C;Accession: A70896

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A;Residues: 1-853 <COL>
A;Cross-references: GB:AL021897; GB:AL123456;
A;Experimental source: strain H37Rv
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: A70896
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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 translation
 PIDN:CAA17207.1;
 not shown
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 PID:e125
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H37RV)

geno

. 268	325 AAAAAAAGGAGQGGLGGQGAGAA
QY 241 QGGLGGQGAGAAAAAAGGAGQGGYGGL	Qy 272AGRGGQGAGAAAAAAGGAGQGGYGGQGAGQGGYGGLGSQGAGRGGLGGQGAGA 324
Qy 194 AGQGGYGGLGGQGA-GQGGYGGLGSQGAGRGGLGGQGAGAAAAAGGAG	Qy 225 LGGQGA-GAAAAAGGAGQGGLGGQGAGAAAAAAAGGAGQGGYGGLGSQG 271
Qy 154 AAAAGGAGQGGYGGLGSQG-AGRGGLGGQ	Qy 166 GGLGSOGAGRGGLGGOGAGAAAAAAGGAGQGGYGGLGGOGAGOGGYGGLGSOGAG-RGG 224
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Qy 58 GQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGLGGQGAGAAA	Oy 103VGQGGLGGQGAGQGAGAAAAAAGGAGQGGYGGLGSQGAG 141
OY 7 GQQMGRIRIRGYGGLGGQGAGQGAGAAAAAAAGGA-CQGGYGGLGSQGAGRG 57	Qy 62GAAAAAAGGAGQGGYGGLGSQGAGRGGLGGQGAGAAAAAGG:102
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<pre>: Sqares, k.; Sulscon, J.E.; Taylor, k.; Whiteleacting the biology of Mycobacterium tuberc ce number: A70500; MUID:98295987 on: A70812</pre>	A; Status: preliminary; nucleic acid sequence not snown; translation not snown A; Molecule type: DNA A; Residues: 1-882 <col/> A; Cross-references: GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAA17640.1; PID:g291689
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, Connor, R.; Davies, R.; Devin, K.; Feltwell, T.; Gentles, S.; Hamlin, N. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, Nature 393, 537-544, 1998	lston, J.E.; Taylor, K.; Whitehead, S.; Barrell biology of Mycobacterium tuberculosis from the 0; MUID:98295987
etical of the state of the stat	R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Deviin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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Db 797 GNGGAGGNGGDALGLVGVGGNGGNAGTGFGANTGGNGGDTTI 838	RESULF 14 B70812 hypothetical glycine-rich protein Rv0834c - Mycobacterium tuberculosis (strain H37RV)
_	
OY 428 GGLGGQGAGAAAVGAGQGGYGGVGSGASAASAASRLSSPQASSRVSSAVSNLVASGPT	Qy 451 vg 452   1   Db 820 AG 821
OY 384 QGGYGGLGSQGAGRGGQGAGAAAAAAGGAGQGGTGGLGGQGYGA 427	Qy 395 AGRGGOGAGAAAAAAGGAGQGGTGGLGGQGYGAGGLGGQGAGAAAAVGAGQGGYGG 450
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hetical glycine-rich protein Rv0833 - Mycobacterium tuberculosis (strain H37RV) cles: Mycobacterium tuberculosis e: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 ession: A70812 e, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon nor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, dream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. e 393, 537-544, 1998 e 393, 537-544, 1998 hors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. le: Deciphering the biology of Mycobacterium tuberculosis from the complete geno session: A70812
 y Match
31.5%; Score 850; DB 2; Length 749;
Local Similarity 36.5%; Pred. No. 1.4e-39;
hes 241; Conservative 21; Mismatches 223; Indels 176;
 751 GGAGGDGGGALGVLG-GMGGDGGDGGEAVAVGIAV---
 384 QGGYGGLGSQGAG-------RGGQGAGAAAAAAGGGGGGGGTGGLGG------QGVGA 427
 194 A-----GQGGYGGLGGQGA-GQGGYGGLGSQGAGRG--GLGGQG--AGAAAAAGGAG 240
 s-references: GB:ALO22004; GB:AL123456; NID:g3261550; PIDN:CAA17639.1; PID:g291
rimental source: strain H37Rv
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 632 ASSPFGIAIAIGGAGAQGGAGTSGATGGAGGDGVFEGIAVLGLGFGGAAGAGGAATGDGA 691
 200 LLALGDGGAGGAATTGTGGAGGAGGKAGLLFGSGGAGGSGGAAGTFGDTGNSGGAGG
 154 AAAAGGAGQGGYGGLGSQG-AGRGGLGGQ------GAGAAAAAA------AGG 193
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 cule type: DNA
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 572 LAAVGGAGAAGGDATSGTGGFGGAGGSARGLIFALGGAGAAGGDASTGVGGPGGPGGTGT 631
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 us: preliminary; nucleic acid sequence not shown; translation not shown
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 20 GGPAGLIGVGGAGGAGGDSAVAGVIGGAGGAGGAALLFGAGGAGGAGGSGGSGAAGGAGG 79
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319
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QY 233 AAAAGGAGQGGLGGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGQGAG 280	Qy 184 GAAAAAAAGGAGQGGYGGLGGQGAGQGGYGGLGSQGAGRGGLGGQGAGA 232	Qy 142RGSGGQGAGAAAAAAAGGAGQGGYGGLGSQGAGRGGLGGQ-GA 183   :			Qy 2 ASMTGGQQMGRIRIRGYGGLGGQGAGQGAGAAAAAAAGGGA-GQGGYGGLGSQG 53	Query Match 31.3%; Score 844; DB 2; Length 778; Best Local Similarity 38.9%; Pred. No. 3.1e-39; Matches 225; Conservative 24; Mismatches 204; Indels 126; Gaps 25;	OY 316 GLGGGG	Qy 285 AAGGAGQGGYGGQGAGQGGYGGLGSQGAGRG 315	Db 704 NGANATTPGAKGGDGGHGGPGAQG-GNGGQGGPGGLAGNLFGQNGIQGVGGSGGKGGAGG 762

Search completed: July 3, 2001, 14:59:45 Job time: 370 sec

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Result
No.
 Title:
Perfect score:
Sequence:
 Minimum
Maximum
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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 Scoring table:
 Run on:
 OM protein -
 Total number of
 Searched:
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33233554
33233554
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and is
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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 | length:
| length:
 hits satisfying chosen parameters:
 Query
Match
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311.1
311.1
311.1
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## ALIGNMENTS

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ניו נ	SPIDROIN 1 (DRAGLINE SILK FIBROIN 1) (FRAGMENT).	
സ	<pre>Nepnila clavipes (Orb spider). Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;</pre>	
4 C)	ntelegynae; Araneoidea; Tetragnathidae;	
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7 2	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	
×	MEDLINE=90384959; PubMed=2402494;	
⋗	Xu M., Lewis R.V.;	
Ŧ	"Structure of a protein superfiber: spider dragline silk.";	
Ľ	Proc. Natl. Acad. Sci. U.S.A. 87:7120-7124(1990).	
υZ	(2)	
× '	MEDLINE=94165058; PubMed=8120021;	
⋗	Beckwitt R., Arcidiacono S.;	
H	"Sequence conservation in the C-terminal region of spider silk	
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## RESULT 2 SPD2_NEPCL В 밁 QY 밁 Qy Query Match Best Local S Matches 314 SPD2_NEPCL P46804; This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and "Isolation of a clone encoding a second dragline silk fibroin. Nephila clavipes dragline silk is a two-protein fiber."; J. Biol. Chem. 267:19320-19324 (1992). - FUNCTION: THIS SPIDER MAJOR AMPULLATE SILK POSSESSES UNIQUE CHARACTERISTICS OF STRENGTH AND ELASTICITY. IT MAY CONSIST OF PSEUDOCRISTALLINE REGIONS OF ANTIPARALLEL BETA-SHEET INTERSPERSED WITH ELASTIC AMORPHOUS SEGMENTS. - SUBUNIT: MAJOR SUBUNIT, WITH SPIDROIN 1, OF THE DRAGLINE SILK. - SUBCELLULAR LOCATION: EXTRACELLULAR. викатуота; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae; Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila. NCBI_TaxID=6915; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last Sequence update) 01-CT-1996 (Rel. 34, Last annotation update) SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT). 01-NOV-1995 (Rel. 01-NOV-1995 (Rel. 01-OCT-1996 (Rel. NON_TER REPEAT REPEAT REPEAT REPEAT REPEAT entities requires a license agreement (See http://www.isb-sib.ch/announce/ Hinman M.B., SEQUENCE FROM N.A. MEDLINE-92406876; PubMed-1527052; or send an email to license@isb-sib.ch). REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT 674 PTNSAALSSTISNVVSQIGASNPGLSGCDVLIQALL SEQUENCE REPEAT 17 GYGPGQQGPGGYGPGQQGPSGPGSAAAAAAAAAAGPGGYGPGQQGPGGYGPGQQGPGRYG GYG----GLGGQGAGQ----GAG-AAAAAAAGGAGQGGYG------GLGSQGAGR--PGQQGPSGPGSAAAAAAAGSGQQGPGGYGPRQQGPGGYGQGQQGPSGPGSAAAAASAASAE 122 ----GGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGLG-GQ----GAGAAAAAGGV----Repeat. P04002; 1WFA. M92913; AAA29381.1; Similarity 51.1 14; Conservative 37 80 122 173 173 214 253 253 284 318 318 360 392 465 Lewis R.V.; STANDARD; 530 36 79 121 121 172 213 252 252 252 359 359 391 488 488 54184 42.5%; Score 1148; DB 1; 51.1%; Pred. No. 1.7e-45; tive 25; Mismatches 139 MW; 2. 5. 6. 7. 11. 11. 12. 14. 15 15 CB9B63779B2C594B CRC64; APPROXIMATE TANDEM There are no restrictions ong as its content is in ₽ 709 139; Length 627; Indels 136; REPEATS and EMBL a collaboration MRI outstation for outstation Gaps 103 62 56 no 9 its

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Tsujimoto Y., Suzuki Y.,
"Structural analysis of the fibroin
surrounding regions.";
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 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
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MEDLINE-94365842; PubMed-7916056;
Mita K., Ichimura S., James T.C.;
"Highly repetitive structure and its gene.";
 Tanaka K., Kajiyama N., Ishikura K., Waga S., Kikuchi A., Ohtomo S.;

"Determination of the site of disulfide linkage between heavy and light chains of silk fibroin produced by Bombyx mori.";

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 MEDLINE-89094868; PubMed-3210244; Mita K., Ichimura S., Zama M., James T. "Specific codon usage pattern and its structure of silk fibroin mRNA."; J. Mol. Biol. 203:917-925(1988).
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 MEDLINE=99296390; PubMed=10366732;
 PIR; S01844; S01844.
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 SECTION OF SILK GLANDS.

DOMAIN: COMPOSED OF ANTIPARALLEL BETA SHEETS. THE STRANDS OF THE BETA SHEETS RUN PARALLEL TO THE FIBER AXIS. LONG STRETCHES OF SILK FIBEROIN ARE COMPOSED OF MICROCRYSTALLINE ARRAYS OF (-GLY-SER-GLY-ALA-)N INTERRUPTED BY REGIONS CONTAINING BULKIER RESIDUES.

THE FIBER IS COMPOSED OF MICROCRYSTALLINE ARRAYS ALTERNATING WITH
 AMORPHOUS REGIONS.
 Evol. 38:583-592(1994).
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149
5244
5260
 Conservative
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5263
5206
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391586
 43.3%;
 28;
 ₩. c
Score 952.5; DB 1;
Pred. No. 3.6e-36;
8; Mismatches 201;
 FIBROIN HEAVY CHAIN.
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 MEDLING-98255987; PubMed-9634230;

A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Cliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

A Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.

A Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

"complete genome sequence.";

Nature 393:537-544(1998).

"SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY; PGRS
 YZ08_MYCTU
O53553;
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV3508 PRECURSOR.
 3048
 RV3508 OR MTV023.15.
Mycobacterium tuberculosis.
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
 SEQUENCE FROM N.A.
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 GQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGSGGGGAGAAAAAAGGAGQGGYGGLGSQGA
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01-JUL-1989
 InterPro; IPR000084; -.

Pfam; PF00934; PE; 1.

Hypothetical protein; Repeat;
SIGNAL
 EMBL; AL022022; CAA17745.1; HSSP; P19972; 1KVD. TubercuList; Rv3508; -.
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 or send an email to license@isb-sib.
 1141
 1081
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 YGGLGSQGA-----
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 ANGGAGGNGGTGGKGGAGGAGTLGVGGSGGTGGDGGDAGSGGGGGGGGGAAGKAGGGGNGG
 NAGYGLTAKAGDGGAAGNGGNGGAGGAGGAGGAGGAGGAGGAGGAGGAGGASTTSIN
 AGGAGQGGLGGQGA-----GAAAAAAGGAGQGGYGGLGSQGA------G
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 -GRGGQGAGAAAAAAGG----AGQGGTGGLGGQGV-----
 24;
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 Score 935; DB 1;
Pred. No. 1.1e-35;
 ; Signal.
POTENTIAL.
HYPOTHETICAL PE-PGRS FAMILY PROTEIN
 PRT;
 Mismatches
 C7B1923D5D0146CD CRC64;
 465
 ----agqgagaaaaaaaaaaaggvrqgg
 220; Indels 206;
 Length 1901;
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 DOMAIN
 Fabales; Fabaceae;
NCBI_TaxID=3885;
 Magnoliophyta; eudicotyledons; core eudicots; Fabales; Fabaceae; Papillonoldeae; Phaseolus.
 01-OCT-1994 (Rel. 30, Last annotation update)
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).
Phaseolus vulgaris (Kidney bean) (French bean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CHAIN
 SEQUENCE
 EMBL; x13596; CAA31932.1;
 or send an email to license@isb-sib.ch).
 SEQUENCE FROM N.A
 HSSP;
 MEDLINE-89091109; PubMed-3208742;
 371
 313
 259
 253
 202
 194
 142
 143
 93
 83
 33
 23
 Local Similarity 47.8
 STRUCTURAL PROTEIN GRP 1.0.
 S01820; S01820.
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 GAGYGGGGGGGGGVAYGGGGE--RGGYGGGQG------GGAG-GGYGAGGEHGIGY 141
 GQGAGQGAGAAAAAAAGGAGQGGYGGLGSQGAGAGAAAAAAAAAAAGGAGQGGYGGLGSQ
 P30129; 4DPV
 33
205
465
 Structural protein;
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 465
359
 30
465
 32.1%;
47.8%;
 36683 MW;
 GLY-RICH.
8 x 22 AA
 Score 866.5;
Pred. No. 5.1
 GLYCINE-RICH CELL PROTEIN 1.8.
 POTENTIAL
 Repeat;
 core eudicots; Rosidae;
 X 22 AA TANDEM REPEATS.
B5C4A9B983B43607 CRC64;
 Mismatches
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 DB 1;
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 Pfam; PF00934; PE;
Hypothetical protei
SEQUENCE 778 AA;
 EMBL; Z80225; CAB02341.1; HSSP; P04002; lATF. TubercuList; Rv2634C; -.
 Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 or send an email to license@isb-sib.ch).
 RV2634C OR MTCY441.04C
 HYPOTHETICAL PE-PGRS FAMILY PROTEIN
 01-NOV-1997
30-MAY-2000
 MEDLINE=98295987; PubMed=9634230;
 SEQUENCE FROM N.A.
 InterPro; IPR001899;
 InterPro;
 7Q34_MYCTU
 421
 207
 371 -- AGGGYGTGGEHGGGYG--GGQGGG-GGYGAGGDHGAAGYGGGEGGGGGGGGGGGGA 425
 54
 N
 SIMILARITY: BELONGS
 SUBFAMILY.
 HGGGYGGGAGGGGYGAGGAH--GGGYGGGGGIGGG
 --GGQGVGAGGLGGQGAGAAAAVGAGQGGYGGVGSG
 LLGDGGAGGQGGPAVAGVLGGMPGAGGNGGNANWFGSGGAGGQGGTGLAGTNGVNPGSIA
 AAGGVGGAASYFGTGGGGGVGGDGAPGGDGGAGPLLIGNGGVGGLGGAGAAGGNGGAGGM
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 ATLVGGTGGVGGATGLIGSGGFGGAGGAAAGVGTTGGVGGSGGVGGVFGNGGFGGAGGLG
 ASMTGGQ-----QMGRIRIRGYGGLGGQGAGQG--AGAAAAAAAGGA-GQGGYGGLGSQG

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 IPR000084;
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 31.3%;
 63131 MW;
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 TO THE MYCOBACTERIAL PE FAMILY; PGRS
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"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
 30-MAY-2000 (Rel. 39, Created)
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WAG22 ANTIGEN PRECURSOR.
WAG22 OR RY1759C OR MTCY28.25C.
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 MEDLINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J.
 MYCTU
 EMBL; 295890; CAB09322.1; -. HSSP; P41140; 2SFA.
 STRAIN-H37
 SEQUENCE FROM N.A.
 Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; My
 Mycobacterium tuberculosis
 WA22_MYCTU
006794;
 InterPro; IPR000084;
 TubercuList; Rv1759c;
 NCBI_TaxID-1773;
 505
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 YGGLGSQG--AGRGGQ--GAGAA-----AAAAGGAGQGGT---GGLGGQGVGAGGLGGQ
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 AAAAGGAGQGGLGGQGAGAAAAAAAGGAGQGGYGGLGSQG-----AGRGGQGAG
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 utes; Actinobacteria; Actinobacteridae;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

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P03211;
 Epstein-barr virus (strain B95-8) (Human herpesvirus Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus. NCBI_TaxID=10377;
 21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-DEC-1998 (Rel.
 EBV
 EBNA-1 NUCLEAR
BKRF1.
 SEQUENCE
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 GGSAGL
 TAAGGAGGAGGAPGLIGNGGNGGESGGTGGVGGAGGNAVLIGNGGEGGIGALAGKSG
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 -GAAAAVGAG-----QGGYGGVGSGASAASAASRLSSPQASSRVSSAVSNLVASGP 486
 FROM N.A
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914 AA;
 ·GAGRGGQGAGAAAAAAGG----AGQGGYGGLGSQGAGRGGLGG-----QGAGA
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01, Last sequence update)
37, Last annotation update)
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 Score 839.5; DB 1;
Pred. No. 1.3e-31;
22; Mismatches 210;
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WAG22 ANTIGEN.
F6953C3DBE8E6AC8
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 Length
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 185;
 Gaps
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 EMBL; V01555; CAA24816.1; -. EMBL; M13941; AAA45889.1; -. PIR; A03773; QQBE31. PIR; S33021; S33021.
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 MEDLINE=86259739; PubMed=3460083;
Sample J., Hummel M., Braun D., Birkenbach M., Kieff E.;
"Nucleotide sequences of mRNAs encoding Epstein-Barr virus
proteins: a probable transcriptional initiation site.";
Proc. Natl. Acad. Sci. U.S.A. 83:5096-5100(1986).
 Gibson T.J., Hatfull G., Hudson G:S. Tuffnell P.S., Barrell B.G.; "DNA sequence and expression of the Nature 310:207-211(1984).
 MEDLINE-84270667; PubMed-6087149;
Baer R., Bankier A.T., Biggin M.D., Deininger P.L., E.
Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C.,
 virus origin-binding protein EBNA 1.
Cell 83:39-46(1995).
 Bochkarev A., Barwell J.A., Pfuetzner Edwards A.M., Frappier L., "Crystal structure of the DNA-binding
 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MEDLINE-96006523; Pubmed-7553871;
 "Subnuclear localization and phosphorylation latent infection nuclear proteins."; Vicology 176:563-574(1990).
 MEDLINE-90266473; Pul
Petti L., Sample C.,
 SEQUENCE OF 1-26 FROM N.A. MEDLINE-86259739; PubMed-1
 SEQUENCE
 3D-structure.
 SUBCELLULAR LOCATION
 100
 Nuclear protein; DNA-binding; Transcription regulation;
 117
 201
 57
 6
 WITH THE NUCLEAR MATRIX.
GLGGQGAGQGGYGGLGSQGAGRGGLGGQGAGAAAAAAAGGAGQGGLGGQGAGAAAAAAAGGAG
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 GRGGSGGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGLGGQGAGAAAAAAAAGGAGQGGYG
 AGGVGQG----
 GPGTGPGNGLGEKGDTSGPEG-----SGGSGPQRRGG-DNHGRGRGRGRGRGGGRPGA
 GAGGAGGAGAG
 PGGSGSGPRHRDGVRRPQKRPSCIGCKGTHGGTGAGAGAGGAGAGGAGAGGGAGAGGGAG
 Similarity
 Conservative
 87
 Barwell J.A., Pfuetzner
 Α,
 PubMed=2161150;
C., Kieff E.;
 352
56427
 30.7%;
 Kieff
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 X.
 18;
 Score 828.5;
Pred. No. 3.
 GLY/ALA-RICH.
, 4D161653E16FC341 CRC64;
 Pred. No. 3.1e
3; Mismatches
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 R.A., Furey W.F.
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 ; DB 1;
 Epstein-Barr virus genome.";
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 http://www.isb-sib.ch/announce/
 152;
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 Epstein-Barr virus
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 Farrell P.J., ., Seguin C.,
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 MEDLINE-98295987; PubMed-9634230; Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.;
SEQUENCE
 Hypothetical protein; SIGNAL 1 3
 EMBL; AL021958; CAA17514.1;
TubercuList; Rv0747; -.
 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
 This SWISS-PROT entry is copyright. It is produced throubetween the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no re
 "Deciphering the biology of Mycobacterium complete genome sequence."; Nature 393:537-544(1998).
 30-MAY-2000
30-MAY-2000
 Pfam; PF00934; PE;
 Bacteria; Firmicutes;
 Mycobacterium tuberculosis.
 RV0747 OR MTV041.21
 HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV0747 PRECURSOR.
 [nterPro
 381
 441 VGAGQG-GYGGVGSGASAASAASRLSSPQASSR 473
 SIMILARITY: BELONGS
 RGRGRGEKRPRSPSSQSSSSGSPPRRPPPGRR 403
 GVRQGGYGGLGSQGAGRGGQGAGAAAAAAGGAGQGGTGGLGGQGVGAGGLGGQGAGAAAA
 QGGYGGLGSQGAGRGGQGAAAAAAAGGAGQGGYGGQGGYGGLGSQGAGRGGLGGQ
 IPR000084;
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ΑĄ,
 STANDARD;
 Corynebacterineae;

 Last sequence up
 Last annotation

 65407
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 Repeat;
 Actinobacteria;
 TO THE MYCOBACTERIAL PE
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 -GRGRGGSGGRGRGSGGRRGRGRER----ARGGSRERA
 RV0747
 HYPOTHETICAL
 Signal
 PRT;
 EA54C9BF45A00F41 CRC64
 It is produced through a collaboration
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 Mycobacteriaceae;
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 (See http://www.isb-sib.ch/announce/
 Actinobacteridae;
 update)
 There are no
 A
 PE-PGRS FAMILY
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 FAMILY; PGRS
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Query Match
Best Local Similarity
Matches 242; Conserv

Conservative

19;

Mismatches

30.4%;

Score 819.5; Pred. No. 9.1

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Length Indels

801; 165;

Gaps

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 Y278_MYCTU STANDARD; PRT; 956877;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV
RV0278C OR MTV035.06C.
MEDINE-98295987; PubMed-9634230;
MEDINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Oliver S., Seeger K., Skelton S., Squares S., Sqares R., Sulston S.
 WYCTU
 Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; MCBI_TaxID=1773;
 SEQUENCE FROM STRAIN-H37RV;
 196
 137
 554
 495
 376
 159
 127
 672
 296
 790
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 73
 17
 LGGQGA------GAAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAAAAAAGGAGQGGYG
 VGGVGGFSNGGATGGAGGAGGAGGLFGAGRERGSGGSGNLTGGAGGAGGNAGTLATGDGG
 QGGYGGLGSQGA--GRGGLGGQGA--GAAAAAAGGVGQGGL--GGQGAGQGAGAAAAAAAGG
 GNGGAGGSGA-PGAGAGGNGGAGGLFGSGGAGGASTDVAGGAGGAGGAGGNAGMLFGAAG
 GYGGLGGQGAGAAAAAAAAGGA-GQGGYGGLGSQ---GAGRGGQGAGAAAAAAAGGAG
 GSPAGAGGIGGAGGNGGLFGAGGTGGAGGGSTLAGGAGGAGGNGGLFGAGGTGGAGSHST
 GQGTIGGVNGGAGGAGGAGGILFGTGGTGGSGGPGATGLGGIGGAG-GAALLFGSGGAGG
 TAPASTSPLHTLQQDVINMVNDPFQTLTGRPLIGNGANGTPGTGADGGAGGWLFGNGGNG
 GNGGNGGASTGGGDGGPGGAGGTGVLIGNGGNGGSGGTGATLGKAGIGGTGGVLLGLDGF
 AGGTGGASRSGGFGGAGGAGGDAGMFFGSGGSGGAGGISKSVGDSAAGGAGGAPGLIGNG
 LLLGEN
 ALLGHH 524
 SGGFSNSGNGGAGGAGGLLVGSGGAGGAGASATGAATGGDGGAGGKSGAFGLGGDGG
 GAAAAAAGGAGQGGTGGLGGQGVGAGGLGGQGAGAAAAVGAGQGGYGG----VGSGASAA
 AAGVSGGAGGAGGDAGLLSLGASGGAGGSGGSSLTAAGVV--GGIGGAGGLLFGSGGAGG
 AAG-GAGQGGLGGQ-----GAGQGAGAAAAAAAAAAAAGGVRQGGYGGLGSQGAGRGGQGA
 GQGAGQGGYGGLGSQGA--GRGGLGGQGAGAAAAAAAAAGGAGQGGL----GGQGAGAAAA
 SGGAGAYGGNGGAGGNAGALLGAAGAGGAGGAGGAYG-GNGGAGGNGGLFANGGAGGPGGF
 AG-----
 AGGATGLSGAFHIGGKGGVGGSAVLIGNGGNGGNGGNSGNAGKSGGA--PGPSGAGGAGG
 SAAASRLSSPQASSRVSSAVSNLVASGPTNSAALSSTISNVVSQIGASNPGLSGCDVLIQ
 -QGGYGGLGSQGA----
 -GAGQGGYGGLGSQG-----AGRGGLGGQGA-----
 Last sequence update)
Last annotation update)
FAMILY PROTEIN RV0278C P
 -GRGGSGGQG------AGAAAAAG-----
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 ----GAAAAAAAGGAG-----
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Matches 219
 Taylor K., Whitehead S., Barrell "Deciphering the biology of Mycob complete genome sequence.";
Nature 393:537-544(1998).
-i- SIMILARITY: BELONGS TO THE MY
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 Hypothetical protein; Repeat; SIGNAL 1 30
 InterPro; IPR000084; - Pfam; PF00934; PE; 1.
 EMBL; AL021930; CAA17353.1; -. TubercuList; Rv0278c; -.
 SEQUENCE
 441
 174
 382
 324
 265
 561
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 681
 228
 Local Si
hes 219;
 17
 SUBFAMILY.
 GYGGLGSQGAGRGGLGGQGA-----GAAAAAGGVG------QGGLGGQGAGQGAGAAAAA
 GYGGLGGQGAGQGAGAAAAAAA---GGAGQGGYGGLGSQGAGGGGGGGAGAAAAAAAGGAGQG
 GSGGHSLVAGGDGGAGGNAGMLALGAAGGAGGIGGDGGTLTAGGIG--GAGGAGGNAGLL
 GVGGSGGAGSSGGAGGAGGAFGAFGTFGAGGTGGHGGFADSSFG-GVGGAGGAGGLFGAGGEG
 QGAGAAAAAGG------GQGGYGGLGSQGAGRGG
 GNGGNGGNGGASAVTGGNGGIGGTGVLIGNGGNGGSGGIGAGKAGVGGVSGLLLGLDGFN
 GRGGLGGQGAGAAAAAAAGG-----AGQGGYGGLGGQGAGQGGYGGL-----
 FGSGGSGGAGGFGFADGGQGGPGGNAGTVFGSG-GAGGNGGVGQGFAGGIGGAGGTPGLI
 AGGAGQGGYGGLGSQGAGRGGSGGQ-----GAGAAAAAAGGAGQGGYGGLGSQGA-----
GTGGDGGHA 869
 LFGAGGTGGAAGSGGSGITTGGGGHGGNAGLLSLGASGGAGGSGGASSLAGGAGGTGGNG
 GQGAGAAAAAAAAAAAGGVRQGGYG-----GLGSQGAGRGGQGAGAAAAAAAGGAG-----
 AAAAAGGAGQGGL-----GGQGAGAAAAAAAGGAGQGGL-----
 APASTSPLHTLQQNVLNVVNEPFQTLTGRPLIGNGANGTPGTGADGGAGGWLFGNGANGT
 GYGGVGSGA
 ALLFGFRGAGGAGGHGGAALTSIQQGGAGGAGGHGGLLFGSAGAGGAGGSGANALGAGTG
 PAGYGGAGGNGGLFANGGAGGAGGFNAAGGNGGLFGTGGTGGAGTNFGAGGNGGNGG
 IGGAGGAGGVSLLIGSGGTGGNGGNSIGVAGIGGAGGRGGDAGLLFGAAGTGGHGAAGGV
 ----QGAGAAAAAAGGAGQGGYGGQGAGQGGYGGLGSQGA------GRGGLGGQGAGAAA
 PGTGAAGGAGGWLFGNGGNGGHGATNTAATATGGAGGAGGILFGTGGNGGTGGIATGAGG
 Similarity 36.0
19; Conservative
 957
 AA;
 30
957
 81905
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 29.9%; Score 807; DB 1; 36.0%; Pred. No. 3.7e-30; tive 21; Mismatches 195
 WW;
 Mycobacterium tuberculosis from
 POTENTIAL.
HYPOTHETICAL |
RV0278C.
 QGGTGGLGGQG---VGAGGLGGQGAGAAAAVGAGQG
 Signal
 MYCOBACTERIAL
 71EBABD417FBA47C
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G
 -GSQGAGR-GGLGG-----
 PE-PGRS FAMILY PROTEIN
 195;
 PΕ
 Length
 CRC64;
 FAMILY;
 Indels 174;
 the
 GGQGA
 680
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 323
 74
 960
 413
 620
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 215
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RESULT
YD25_MY
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 Query Match
Best Local Similarity
 Matches
 YD25_MYCTU
Q10637;
Q1-OCT-1996
Q1-OCT-1996
Q1-OCT-1996
 MEDLINE-98295987; PubMed-9634230;

COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harri
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Badries R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Oliver S., Osborne J., Ouail M.A., Rajandream M.A., Rogers J.,

Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston

Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";

Nature 393:537-5441998).
 MYCTU
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 DOMAIN
SEQUENCE
 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence
30-MAY-2000 (Rel. 39, Last annotation
HYPOTHETICAL PE-PGRS FAMILY PROTEIN
RV1325C OR MTCY130.10C.
 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 Hypothetical protein; Repeat; Signal SIGNAL 1 30 POTENTI
 InterPro; IPR000084; Pfam; PF00934; PE; 1
 HSSP; P19972; 1KVD.
TubercuList; Rv1325c; -.
 EMBL; 273902; CAA98089.1;
 SEQUENCE FROM N.A.
 NCBI_TaxID-1773;
 275
 182
 113
 70
 10
 SIMILARITY: BELONGS
GGGGGLFSNGGAGGAGGFGVSGSAGGNGGTGGDGGIFTGNGGTGGTGGTGNQLVGGEG
 LFGNGGAGGAGGDGPGNGAAGGAGGAGGLLFGSGGAGGPGGVGNTGTGGLG----GDGGAA
 GAGQGGYGGLGSQGAGRGGLGGQ------GAGAAAAAGGVGQGGLGGQGAGQGAGAAA 121
 LGRPLI-GNGANGAPGTGQ-----
 MGRIRIRGYGGLGGQGAGQGAGAAAAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAAAAAAG
 GLFGAGGIGGAGGPGFNG-GAGGAGGRSGLFEVLAAGGA--GGTGGLSVNG
 Conservative
 STANDARD;
 603
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603
 29.0%;
 Last sequence update)
Last annotation update)
FAMILY PROTEIN RV1325C P
 TO THE MYCOBACTERIAL PE
 ¥.
 Score 782.5; DB 1
Pred. No. 3.4e-29;
 POTENTIAL.
HYPOTHETICAL
RV1325C.
GLY-RICH.
 4F9BCB82B07AE964
 Mismatches
 AGGAGGLLYGNGGAGGSGAPGQ-AGGPGGAAG
 603
 PE-PGRS
 202;
 PRECURSOR
 CRC64
 FAMILY;
 Indels
 Length
 FAMILY
 Mycobacterium
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RESULT 12
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 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
 01-MAR-1989 (Rel.
01-MAR-1989 (Rel.
01-AUG-1992 (Rel.
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 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteric Solanales; Solanaceae; Petunia.
 GLYCINE-RICH
 GRP1_PETHY P09789;
 SIGNAL
 Condit C.M., Meagher R.B.;
 SEQUENCE
 NCBI_TaxID=4102;
 Petunia hybrida (Petunia)
 HSSP; P30129; 4DPV
 454
 328
 394
 wall;
 GNGGNGGVGSAPGKGGAGGTAGLLGLNGSPGLS 603
 RQGGYGGLGSQG-AGRGGQGAGAAAAAAGGAGQGGTGGLGGQGVGA-GGLGGQGAGAAAA
 GLGGQGAGAAAAAGGAGQGGLGGQGAGAAAAAAAGGAGQGGYGGLGSQGA-----GRG
 VGAGQGGYGGVGS--GASAASAASRL---SSPQAS 471
 GAGGAGGLGIAGDGGNGGKG-----GKAGMYGNGGDGGAGGASVVANGGYGGSGGNATLI
 GFGASSADQMAGGIGGSGGSGGAAKLIGDGGAGGTGGDSVRGAAGSGGTGGTGGLIGDGG
 GAGGAGGNAGILFGAGGIGGTGGTGLG-APDPGGTGGKGGVGGIGGAGALFGPGGAGGTG
 AGGAGGTG I EFGS VGGAGGAG
 GQGAGAAAAAAGG-AGQGGYGGQG--AGQGGYGGLGSQ----GAGRGGLGGQGAGAA-AA
 X04335; CAA27866.1;
 FROM
 41
384 /
 Structural_protein; Repeat; Signal
 A26099.
 OF REPEATS, F1 AND F2, EACH REPEAT CONTAINING
 28
 N.A.
 AA;
 STANDARD;
 WALL
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Last annotation update)
 Created)
 STRUCTURAL
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 -GNAAGLSGAGGAGGAGGFGETAGDGGAGGNAGLLNGDG
PROTEIN 1.
GLY-RICH.
; C8541C549417D18C CRC64;
 GLYCINE-RICH
 PRT;
 PROTEIN 1 PRECURSOR
 eudicots; Asteridae;
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 There are no restrictions
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Query Match Best Local Sir Matches 197;

Similarity

27.3%; 46.8%;

Score 736; Pred. No. 3

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DB 1; Length 384;

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 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ELN.
 EMBL; U08210; AAA80155.1; -. HSSP; P04002; 1WFA. MGD; MGI:95317; Eln.
 MEDLINE 95130069; PubMed-7829060; Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.; "Use of an intron polymorphism to localize the tropoelastin mouse chromosome 5 in a region of linkage conservation with
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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 Genomics 23:125-131(1994)
 chromosome
 SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Lung;
 Mus musculus (Mouse)
 ELS_MOUSE
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 NCBI_TaxID-10090;
 277
 144
 383
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 331
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 157
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 FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA A FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA A NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLE SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETH INTO AN EXTENSIBLE 3D NETWORK.
SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
FIM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
 G 454
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 GGGAGSGGGFGAG-----GGVGG-GAGA------GGGVGGGGGFGG-----GGGGGGVG
 AGGAGQGGYGGLGSQGAGRGGLGGQGAGAAAAAAAAGGAGQGGYGGLGGQGAGQGGYGGLG
 GAAGGVGGGGFGGGGGGGGGGGGGGGGGGGGG
 SQGAGRGGLGGQGAGAAAAAGGAGQGGLGGQGAGAAAAAAAGGAGQGGYGGLGSQGAGRGG
 AAAAGGYGQGGLGGQGAGQGAGAAAAAAAGGAGQGGYGGLGSQGAGRGGSGGQGAGAAAAA
 GCGFGRRGCGGGRFGGRGPSFGRGRGAGGGFGGGAGGGGLG----GGGGLGGGG---
 383
 STANDARD;
 34, Last sequence update)
34, Last annotation updat
(TROPOELASTIN).
 34, Created)
 Craniata; Vertebrata; Sciurognathi; Muridae;
 PRT;
 860
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 Euteleostomi;
 Murinae;
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TOGETHER
 a collaboration –
MBL outstation –
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 453
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 184
 93
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 396
 228
 216
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RESULT 14

GRP_ARATH STANDARD; PRT; 338 AA.

ID GRP_ARATH STANDARD; PRT; 338 AA.

AC P27483;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN PRECURSOR.
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 Query Match
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Matches 226
 Structural
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 SEQUENCE
 This SWISS-PROT entry is copyright. It is produced through a control of mininformatics and the EMBL
 Quigley F., Villiot M.L., Mache R.;
"Nucleotide sequence and expression
gene from Arabidopsis thaliana.";
Plant Mol. Biol. 17:949-952(1991).
 STRAIN=CV. COLUMBIA; MEDLINE=92003708; Pu
 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
 SEQUENCE FROM N.A.
 -!- FUNCTION: RESPONSIBLE FOR PLASTICITY OF THE -!- SUBCELLULAR LOCATION: CELL WALL (POTENTIAL).
 414
 699
 362
 647
 305
 588
 247
 533
 191
 473
 413
 106
 353
 293 VAGAGGKAGYPTGTGVGSQAAAAAAKAAKYGAGGAGVLPGVGGGGIPGGAGAIPGIGGIA
 759
 60
 -AAAAAAGGAGQGGYGGLGSQGA-------GRGGLGGQG--AGAAAAAA
 GAGTPAAAAAAKAAAKAAKYGAAGGLVPGGPGVRLPGAGIPGVGGIPGVGGIPGVGGPGI
 GAG---AAAAAAGGAGQGGYGGLGS-------QGAGRGGLGG-QGAGAAAAAGGVGQ
 IRGYGGLGGQGAGAAAAAAAGGAGQGGYGGLG-SQGAGRGG------Q
 GLGAGGLGAGGLGAGG-GVSPAAAAKAAKYGAAGLGGVLGARPFPGGGVAA
 QGGTGGLGGQGVGAGGLGGQGAGAAAAVGAGQGGYGGV-----GSGASA 457
 GAGAGVPGFGAGAVPGSLAASKAAKYGAAGGLGGPGGLGGPG-----GLGGPGGLGG
 QGAGAAA-AAAGGAGQGGYGGLGSQGAGAGGGGQGAGAAAAAAG-GAGQGGYGGQGAGAGAGGGGY
 AGGAGQGGYG-GLGG--QGAGQGGYGGLGSQGAGRGGLGGQGAGAAAAAG-GAGQGGLGG
 GGPGIVGGPGAVSPAAAAKAAAKYGARGGVGIPTYGVGAGGFPGYGVGAGAGLGGAS
 GG---LGGQGAGQGAGAAAAAAGGAGQGGYGGLG--SQGAGRGGSGGQGAG-----
 QG----AGQGAGAAAAAAAAGGVRQ---GGYGGLGSQGAGRGGQGAGAAAAAAAGGAG
 AGSPAAAKSAAKAAAKAQYRAAAGLGAGVPGFGAGAGVPGFGAGAGVPGFGA-GAGVPGF
 AKAAAKAGLGPGVGGVPGGVGGIPG----GVGVGGVPG-GVGPGGVTGIGAGPGGLGG
 AGVPGRVAGAAPPAAAAAAAKAAAKAAQYGLGGAGGLGAGGLGAGGLGAGGLGAG
 226;
 Similarity
 protein;
 860 AA;
 Conservative
 PubMed=1912511;
 860
71955
 Institute
 Repeat;
27
 27.0%;
 W.
 23;
 Signal; Connective POTENTIAL. ELASTIN.
 Score 729.5;
Pred. No. le
 OCOBESAAE1EDD7F1
 Mismatches
 of a novel
 1e-26;
 179;
 tissue
 glycine-rich
 CELL
 Indels 103;
 Length
 WALL
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 (POTENTIAL).
 a collaboration
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 Gaps
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Matches 192
SEQUENCE FROM N.A.

MEDLINE-90275605; PubMed-2190691;
Mehrel T., Hohl D., Rothnagel J.A., L
Cheng C., Lichtl U., Bisher M.E., Ste
Yuspa S.H., Roop D.R.;
"Identification of a major keratinocy
loricrin.";
Cell 61:1103-1112(1990).
 LORI_MOUSE
P18165;
01-NOV-1990
01-NOV-1997
 MOUSE
 SEQUENCE
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentla; Sclurognathi; Muridae; Murinae; Mus
NCBI_TaxID-10090;
 the European Bloinformatics Institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 Cell wall; Structural protein; Repeat; Signal. SIGNAL 1 20 POTENTIAL.
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 EMBL; M34398; AAA39444.1; -. EMBL; U09189; AAA82152.1; -. PIR; A35628; A35628.
 differentiation-specific expression."
J. Biol. Chem. 270:10792-10799(1995).
 STRAIN-BALB/C;
 SEQUENCE
 Keratinocyte.
 HSSP; P10968; 1WGC.
 "The proximal promoter of the mouse functional AP-1 element and directs
 MEDLINE-95256248;
414
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 25 GAGQGAGAAAAAAAGGAGQGGYGGLGSQGAGGGGGGGAGAAAAAAGGAGQGGYGGLGSQGA 84
 GLUTAMYL) LYSINE ISODIPEPTIDE BONDS.
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SUBUNIT: MONOMERS ARE CROSSLINKED BY DISULFIDE AND N-(GAMMA-
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37.7%;
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 1 MASMTGGQQMGRIRIRGYGG......GLSGCDVLIQALLGHHHHHH
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27.5	27.7	27.7	27.7	28.1	28.3	28.4	28.7	28.9	29.0	29.4	29.5	29.7	30.0	30.0	30.1	30.1	30.3	30.4	30.6	30.8	30.9	31.0	31.2	31.4	31.4
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## ALIGNMENTS

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 O 046171 PRELIMINARY; PRT; 544 AA.

C 046171;
C 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
I 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
E SPIDROIN 1 (FRAGMENT).
S Nephila clavipes (Orb spider).
C Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Arachaneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila Clavipes (Orb spider).
C NCB_TaxID=6915;
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 Beckwitt R., Arcidiacono S., Stote R.;
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MEDLINE=90384959; PubMed=2402494;
Xu M., Lewis R.V.;
 Arcidiacono S., Mello C., Kaplan D., Cheley S., Bayley H.; Purification and characterization of recombinant spider silk expressed in Escherichia coli.", appl. Microbiol. Biotechnol. 49:31-38(1998).
 "Structure of a protein superfiber: spider dragline silk."; Proc. Natl. Acad. Sci. U.S.A. 87:7120-7124(1990).
 SEQUENCE FROM N.A.
 SEQUENCE OF 449-544 FROM N.A. MEDLINE-98148687; PubMed-9487707;
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 Score 2555; DB 5;
Pred. No. 5.8e-143;
Mismatches
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 O46172 PRELIMINARY; PRT; 617 AA.
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Nephila clavipes (Orb spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
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MEDLINE-94165058; PubMed-8120021;
Beckwitt R., Arcidiacono S.;
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 121
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 301
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 257
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 U37520; AAC04504.1;
e conservation in the C-terminal region of spider silk (Spidroin) from Nephila clavipes (Tetragnathidae) and arius (Araneidae)."; Chem. 269:6661-6663(1994).
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 EMBL; AF027735; AAC14589.1; InterPro; IPR000817;
 "Spider minor ampullate silk proteins contain new repetitive sequences and highly conserved non-silk-like 'spacer regions'."; protein Sci. 7:667-672(1998).
EMBL; AF027735; AAC14589.1; -.
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MEDLINE-98200471; PubMed-9541398;
Colgin M.A., Lewis R.V.;
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Conservative

23; Mismatches Score 1397; DB 5; Pred. No. 7.8e-75;

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 MEDLINE-96178678; PubMed-8600519; Guerette P.A., Ginzinger D.G., We "Silk properties determined by gl fibroin gene family."; Science 272:112-115(1996).
 ADF-3.
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Eukaryota; Metazoa; Arthropoda; Chelicer
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 NCBI_TaxID=45920;
 946
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FIBROIN.
 Antheraea pernyi (Chinese oak silk moth).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

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Bombycoidea; Saturniidae; Saturniinae; Antheraea.
 EMBL; U47855; AAC47010.1;
InterPro; IPR001419; -
PRINTS; PR00210; GLUTENIN.
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Sezutsu H., Tamura T. Characterization of
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Sezutsu H., Tamura T.,
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 Score 1099; Di
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01-OCT-2000
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 Antheraea pernyi.";
Submitted (AUG-1998) to the
EMBL; AF083334; AAC32606.1;
SEQUENCE 2639 AA; 216056
 1560
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 184 GAAAAAA ----- AGGAGQGGYG-----
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 gene.";
Science 287:1477-1479(2000)
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MEDLINE=20156766; PubMed=10688794;
Hayashi C.Y., Lewis R.V.;
"Molecular architecture and evolut
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 1278
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 27B6F45339FD20A5
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 197; Indels 172;
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Matches 238; Conservative 14
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
 EMBL; AL022022; CAA17749.1; -.
TubercuL1st; Rv3512; -.
InterPro; IPR002202; -.
PROSITE; PS00318; HMG_COA_REDUCTASE_2; UNKNOWN_1.
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PGRS-FAMILY PROTEIN (FRAGMENT).
 MEDLINE-98295987;
 SEQUENCE FROM N.A.
 Mycobacterium tuberculosis
 RV3512 OR MTV023.19.
 670
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 InterPro;
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 SEQUENCE
 MEDLINE-98153262; PubMed=9480768; Hayashi C.Y., Lewis R.V.;
 Araneomorphae; E
NCBI_TaxID=6915;
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 Eukaryota; Metazoa;
 Nephila clavipes (Orb spider).
 InterPro; IPR000087; -
 456
 540
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 Similarity
 871 AA;
 Conservative
 Entelegynae;
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044358 PRELIMINARY; PRT; 871 AA. 044358; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update) FLAGELLIFORM SILK PROTEIN (FRAGMENT).
 "Evidence from flagelliform silk cDNA for the structural basis elasticity and modular nature of spider silks.";
J. Mol. Biol. 275:773-784(1998).
EMBL; AF027972; AAC38846.1;
 304 GGAGPGGYGPGGAGPGGYGPGGAG----PGGYGPGGTGPGGYGPGGYGPGGAGPG
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Nephila.
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 Gaps
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A COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

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A Davies R., Devlin K., Feltwell T., Gentles S., Murphy L.,

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A Davies R., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

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A Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,

Taylor K., Whitehead S., Barrell B.G.;

Tocciphering the biology of Mycobacterium tuberculosis from the

"Complete genome sequence.";

Nature 393:537-544(1998).

EMBL; ALO22022; CAA17751.1; -.

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 01-JUN-1998 (TrembLrel. 06, 01-JUN-1998 (TrembLrel. 06, 01-JUN-2000 (TrembLrel. 14, PGRS-FAMILY PROTEIN.
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 178
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last annotation
FLAGELLIFORM SILK PROTEIN (FRAGMENT).
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InterPro; IPR000087; -.
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MEDLINE-20156766; PubMed-10688794;
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Science 287:1477-1479(2000)
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 2249
2249
 AA;
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-GAGAAAAAAAGG----
 174871 MW;
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 Nephila clavipes (Orb spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
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 329
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Best Local Similarity 34.
Matches 258; Conservative
 EMBL; AL022022; CAA17744.1; -
HSSP; P00778; 2ULL.
Tubercullst; Rv3507; -
InterPro; IPR000084; -
InterPro; IPR002173; -
Pfam; PF00934; PE; 1.
 01-JUN-1998 (TrEMBLrel. 0
01-JUN-1998 (TrEMBLrel. 0
01-GCT-2000 (TrEMBLrel. 1
PGRS-FAMILY PROTEIN
RV3507 OR MTV023 14
 MEDLINE-98295987; pubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
 053552
 Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; MyCBI_TaxID=1773;
 SEQUENCE FROM N.A.
 Mycobacterium tuberculosis.
 ProDom; PD001223; -; 1.
PROSITE; PS00583; PFKB_KINASES_1;
SEQUENCE 1381 AA; 110624 MW; (
 870
 493
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 644
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 11
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 33.0%;
 15,
 888
 512
25;
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Last sequence update)
Last annotation update)
 Score 892;
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 ; UNKNOWN_2.
CA09676BD07F6482 CRC64;
 a; Actinobacteridae;
Mycobacteriaceae; M
 1381
 2; DB 2;
. 4.3e-45;
 -----GLGGQGVGAGGLGGQGAGAA
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 ------GSGPGGAGGA
 Length 1381;
Indels 242;
 Mycobacterium.
 Sulston J.E.,
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01-OCT-2000 (TrEMBLrel.
 Pinctada fucata.
Eukaryota; Metazoa; Mo.
Pterioidea; Pteriidae;
 MEDLINE-97320490; PubMed-9177341;
Sudo S., Fujikawa T., Nagakura T.,
Nakashima K., Takahashi T.;
"Structures of mollusc shell framework proteins.";
Nature 387:563-564(1997).
 SEQUENCE FROM N.A.
 INSOLUBLE PROTEIN.
 002402
 NCBI_TaxID=50426;
 501
 859 FGGNTTSGASGSGGNGGNAGTAG
 492
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 287
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 184
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 149
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 107
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 APIGGGAGGTGGSGGHAGKGGAGGIGAQGTTITVPGNGGNAGDGGNGGNAGAGGNGGSGD
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 PRELIMINARY;
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Last sequence up
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 -QGGTGGLGGQGVGAGGLGGQGAGAA
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 AAAAAAAGGVRQGGYGGLGSQGA
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 -----AGAA
 -AGRGGLGGQ----GAGA
 ----QGAGAAAAA
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Matches 257
 O53435 PRELIMINARY; PRT; 767
O53435;
O1-JUN-1998 (TrEMBLrel. 06, Last sequence of the control of
 EMBL; D86074; E
SEQUENCE 738
 MEDLINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia Badcock K., Basham D., Brown D., Chillingworth T., Connor
 STRAIN-H37RV;
 SEQUENCE FROM N.A.
 113
 173
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257; Conserv
 Conservative
 33.0%; Score 890.5; DB 41.7%; Pred. No. 3e-45;
 707
 461
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Last sequence update)
Last annotation updat
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 Mismatches
 a; Actinobacteridae;
Mycobacteriaceae; M
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Best Local :
 Q9GUB5;
Q9GUB5;
Q1-MAR-2001
01-MAR-2001
01-MAR-2001
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., H
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murph
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers
Rutter S., Seeger K., Skelton S., Squares S., Squares R., Su
Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from
complete genome sequence.";
Nature 393:337-544(1998).
REMBL, AL021897; CAA17203.1; -.
 Pfam; PF00934; PE; 1.

ProDom; PD001223; -; 1.

PROSITE; PS00583; PFKB, KINASES 1; UNKNOWN 1.

SEQUENCE 767 AA; 62469 MW; 1F5F3B9F6E2014F8
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 Galleria
 FIB-H
 HEAVY-CHAIN
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42.2%; Pred.
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 22;
 Mismatches
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 880; DB 2;
No. 1.3e-44;
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 Eukaryota; M
Pterygota; N
Pyraloldea;
 TISSUE-POSTERIOR SILK GLAND;
ZUROVEC M., KOĞITİK D., Yang C., Sehnal F.;
"Heavy-chain fibroin of Galleria mellonella L.
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ
EMBL; AF095239; AAG10393.1; -.
NON TER 1468
 1004
 Pyraloidea; Pyralidae;
NCBI_TaxID=7137;
 468
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eree
 Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Pyralidae; Galleriinae; Galleria.
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 ----TNSAALSSTISNVVSQIGAS
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Nature 393:537-544(1998).

EMBL; AL021246; CAA16067.1; -. Tate-For. Taponogad. -.
 Prodom; PD001223; -; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
PROSITE; PS01287; RTC; UNKNOWN_1.
SEQUENCE 1660 AA; 133124 MW; 3A889CE12C0
 Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 053215;
01-JUN-1998
 053215
 SEQUENCE FROM N.A.
 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
 RV2490C OR MTV008.46C
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InterPro; IPR000228; -.
InterPro; IPR002173; -.
649
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Pred. No. 1.2e-43;
2; Mismatches 175;
 3A889CE12C0FA945 CRC64;
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